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Copyright (c) 1993 - 2000 Comp
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4 130713 MA
5 602094862
7 000-HT036
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8 346420 MA
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ALIGNMENTS	BP463964 BG727939 AAB71419 AB71419 AB780309 BF890309 BF8903081 BE156600 BF883081 BE156600 AI006678 AQ976378 BA976378 BA976378 BA98364736 AW480438 AQ996374 BF610846 BF441578 BF8411578 BF8411578 BF8416592 AZ96598 BF747241 AAB71638 BF4611310 BF1220929 BI220929 BI230869 BI219321 AW603701 BG8178100 BI2178100 BI318100
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RESULT 1
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KEYWORDS COMMENT REFERENCE SOURCE TITLE AUTHORS ORGANISM MEDLINE JOURNAL Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-HT0513-150 300-117-f10&t3=2000-03-15&t4=1)
Seq primer: puc 18 forward Dias Neto,E., Garcia Correa,R., verjovski ni Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bord Goldman,G.H., Carvalho,A.F., Matsukuma,A., E Brunstein,A., deOliveira,P.S., Bucher,P., Jc ,M.J., Soares,F., Brentani,R.R., Reis,L.F., Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, BE168072 569 bp mF QV3-H70513-150300-117-f10 BE168072 BE168072.1 GI:8630793 EST. $\operatorname{Simpson, A.J.}$ Shotgun sequencing of the human transcriptome with ORF expressed Tel: +55-11-2704922 Fax: +55-11-2707001 20202663 sequence tags Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens (bases 1 to 569) Natl. Acad. Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., a Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Sci. U.S.A. Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. HT0513 Homo sapiens cDNA, mRNA sequence 97 (7), 3491-3496 (2000) 01509-010, Sao Paulo-SP, 21-JUN-2000

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EST.
                                                            Single pass sequencing. Bases ov v0.980904.e. Vector identified
                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                           Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                           Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennet and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                         pig.
Sus scrofa
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FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                     Email: smith@email.marc.usda.gov
single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                           Design and use of two pooled EST discovery in swine
                              PCR PRimers
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/dev_stage="Adult"
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Library made from pooled tissue from day 1
and 30 embryos."
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/db_xref="taxon:9823"
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/lab_host="DH10B"
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Pred. No. 4.1e-46;
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day 11, 13, 15, 20,
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GGACCTTGGCTTGCGTTGCGGTCATCTTCTCCCTGCTGCTCGTGGTGGTCCGGAC

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1434 gecetatggtgtggeagtgggtgteecetectecgteetggtegtggtetteeagae
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                                                                                                                                                                                                                                                                CATTGTCAAACTTGGGGAACTCTTCCATGACCTGCCCAAGGCGGTCCTGGCAGCCATCAT
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                                                                         CAATCGGGCGGATCTGCTTATCTGGCTGGTGACCTT-CACGGCACCATCTTGCTGAACCT
                                                                                                  CATTGTGAACCTGAAGGCATGCTGAGGCAGCTCAGCGACATGCGCTCCCTCTGGAAGGC
                                                                                                                                                                                           cyctytcaatctcaagaactccctcaagcaactcaccgacccctactacctytygaggaa 1373
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                                                                                                                                                                                                                                                                                                                                                              GAGCACCGGGGGCAACTCGCAGGTTGCTGGAGCCATCTCTTCCCTTTTCATCCTCCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4849228"
/clone_lib="NIH_MGC_108"
/clone_lib="NIH_MGC_108"
/clone_lib="NIH_MGC_108"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB/; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT prinding. Directionally cloned
into EcoRI/XhoI sites using the following 5′ adaptor:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.8e-31;
0; Mismatches 360;
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ttggctccttctttaaaattcatgtcatttgctgtgcgctttc-tgtcactctggctgtg 1191
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246; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-CMI&t2-CM1-ET0042-
130600-264-h04&t3-2000-06-13&t4-1)
Seq primer: puc 18 forward
Lich Conference of the property of the conference of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification low stringency conditions. 92 c 92 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="ET0042"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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96.5%;
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                                                                                                              Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 1246)
Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Aklyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome research. 10 (11), 1757-1771 (2000)
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new common research. 10 (10), 1617-1630 (2000)
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Mus musculus adult male colon cDNA, RIKEN full-length
library, clone:9030623B18, full insert sequence.
                         Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama.
                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                             Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                       RIKEN Yokohama Institute;
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mmalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RIKEN Genome Exploration Research Group Phase II Team and
Japan (E-mail:genome-res@gsc.riken.go.jp,
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-AGCTCCACAGAAAATGACTCGTTCATAGAGGAGAAAGTAATGGTGGCTGCATCAGTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.j
further details.
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/db_xref="GI:12858334"
/translation="mwwpDrCTpQrLLERSLRRRTDITRHSWTISKGVVASWLPAYKI/translation="mwwpDrCTpQrLLERSLRRRTDITRHSWTISKGVVASWLPAYKIKEWLLSDIVSGISTGLWAVLOGLAFALLVNIPPAYGLYAAFEPVITYEFLGTTSRHISVGEPVLSMYVGVVTRVVSDPRASSELSSSSTENDSFIEEKVMVAASVTVLSGIIQLLLGVLQVGFVVIYLSESLISGFTTAAAIHVLVSQLKFMLQLFVPAYSDPFSIFKVLESVLGVLQVGFVVIYLSESLISGFTTAAAIHVLVSQLKFMLQLFVPAYSDPFSIFKVLESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="colon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
239. .1069
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/strain="C57BL/6J"
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/db_xref="MGD:MGI:1918793"
/clone="9030623B18"
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                                                                                                                                                                                                                                                                                                                                                                                     84112,
Tel: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
University of Utah
University of Utah
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                                                                                                                                                                                                                                                                            Seq primer: CGTTGTAAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                 /note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/).
                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0116E10"
                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                           /sex="Male"
                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
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130773 MARC 1PIG Su
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                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                               1 (bases 1 to 586)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Stone, R.T., Heaton, M.P., Grosse, W.M., Benne
                                                        Single pass sequencing. Bases ov v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                           EST discovery in swine
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                                                                                                                                                                                                                                                                              and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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Similarity 75.5%;
25; Conservative
                  PCR PRimers
                                       -minmatch 12 options
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Seq pri
                           Mus musculus
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                                                                              mRNA sequence.
BF578820
                                                                                                    BF578820 857 bp mt
602094862F1 NCI_CGAP_Co24
    Eukaryota;
Mammalia; |
                                                                 BF578820.1
                                           house mouse
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/db_xref="taxon:9823"
/clone_lib="MARC lpig"
/tissue_type="pooled"
/lab_host="DH108"
/note="Vector: pcMV SPORT6; Site_1: XbaI; SiLibrary made from pooled tissue from day 11, and 30 embryos."
3 a 169 c 163 g 141 t
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 Eutheria;
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Pred. No. 2.5e-24;
0; Mismatches 249;
                                                                                                        Mus
Craniata; Ver
Sciurognathi;
                                                                                                        musculus
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Vertebrata;
thi; Muridae;
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  day 11, 13, 3
             Euteleostomi;
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Best Local S
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ctcaatgctcgctacatgcacaagattcgcttccccatccctacagagatgattgtggtg
                                                                                                                                                                                                                        ggcctgcagatcctgatttcggtgctcaagtacatcttcggactgaccatcccctctac
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                                                       AACATCGCAGACCTTGTGACATCTGTGATTATTCTAGTGGTCGTCTCTCTTAAAGAA
                                                                                       aacatcgcctcgctcatcttcgctctcatcagcggtgccttcctggtgctggtgaaggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 857)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Plate: LLAM9774 row: l column:
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/db_xref_"taxon:10090"
/clone="IMAGE:4209183"
/clone="lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="Oloned unidirectionally. Primer: Oloned unidirectionally. Primer: Ol. Site_2: Sall; Cloned unidirectionally. Primer: Ol. Site_2: Sall; Cloned unidirectionally. Primer: Ol. Site_2: Note: tsize 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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Best Local Similarity
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                               gctatgcactggcccaggtcatggacactgacatttatgtgaatcccaagacctataata 1564
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     ACTCTGTCCTGGGGCAGGTGCCAGACACGGATATTTACAGAGATGTGGCAGAGTACTCAG
                                                                                    tggcagtgggtgtcgccttctccgtcctggtcgtggtcttccagactcagtttcgaaaatg 1504
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                                                                                                                                                                                                     TGAAGGGCATGCTGAGGCAGCTCAGCGACATGCGCTCCCTCTGGAAGGCCAATCGGGCGG
                                                                                                                                                                                                                                                                     TGGGGAACTCCTTCCATGACCTGCCCAAGGCGGTCCTGGCAGCCATCATTGTGAACC 60
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10614 row: g column: 09
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG680597 611 bp mRNA ESI VALUE TANA 602629036F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753952 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: LLAM10614 row: g column: High quality sequence stop: 610.
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BG680597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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1 (bases 1 to 611)
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                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="squamous cell carcinoma"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: skin; vector: pCMV-SPORR6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 163 c 181 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4753952"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Ludwig Institute for Cancer Research
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QVO-HT0368-310300-181-f03 HT(
BE156730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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300-181-f03&t3=2000-03-31&t4=1)
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BB605137 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030008K16 5', mRNA sequence.
BB605137
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URL:http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
Sakai,K., Sasaki,D., Sato,K., Shibata,Y., Shibata,Y., Shinata,Y., Shinata,Y., Shinata,Y., Shinata,Y., Shinata,Y., Shinaki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
,T., Toya,T., Watchiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                  trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Carninci,P. and Hayashizaki,Y.
                                                                                                                          High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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                                                                      visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTGGTGCTCCTCAGCCAAGTTCAAAGCCTATGTGTTGGGGGGTGTCGCCTGTGCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAACCAGCCCAGGCCCCGCTACGTGGTATATAGAGCTGGGTAATCCCTCTCCCTCTTC 146
                                   USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                          Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                BG732794 521 bp
346420 MARC 1PIG Sus
BG732794
                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                          Sus scrota
                                                                                                                                                                                                                                                                                                                                                                   BG732794.1
Single pass sequencing.
                   Email: smith@email.marc.usda.gov
                                                                                                                 Contact: Smith TPL
                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA
                                                                                                                                                                                                                                                   1 (bases 1 to 521)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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80.0%;
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Bases
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called
and alt_trimmed with
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Sus.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtctgggcttcatgcagtttggctttgtggccatctacctctccgagtccttcatccggg
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                                                                                                                                                                              GGGAGCTACTCACGCTCATCGGGGCCACAGGCATCTCCTACGGC 519
                                                                                                                                                                                                                                                                                        GGAATCTGCCCAAGACTGTAGTCAACACCTTGGTCACTGCAGTTGTGGCAGGGTTGGTGC
                                                                                                                                                                                                                                                                                                               aaaacctcccccacaccaacatcgcctcgctcatcttcgctctcatcagcggtgccttcc 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCTAGGCGGTGCAGCTGGCCTCTGCACTCAGTGTCCTAGTGGGCCTCTTTCAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACCTTTGCTGTCATGTCTGTGATGGTGGGCAGTGTGACAGAATCGCTGGCCCCAGATG 67
                                                                                                                                                                                                                                   TCGTGCTGGTGAAGCTATTGAACAACAAGCTGCAGAAACATCTGCCCGTGCCACTCCCCG
                                                                                                                                                                                                                                                   tggtgctggtgaaggagctcaatgctcgctacatgcacaagattcgcttccccatcccta
                                                                                                                                                                                                                                                                                                                                             TCCATCTGAGCAGCCGCTCTGGGCCACTGTCCCTCATCTATACAGCACTGGAGGTCTGCT
                                                                                                                                                                                                                                                                                                                                                                    tgaccatcccctcctacacaggcccagggtccatcgtctttaccttcattgacatttgca 736
                                                                                                                                                                                                                                                                                                                                                                                                 GCTATACCACAGCCGCGTCCGTGCAGGTCTTCATCTCACAGCTCAAGTATGTGTTTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGGGCCTGGTCCACTTTGGCTTCGTGGTCACCTACTTGTCAGAGCCTCTGGTCCGTG
                                         UI-M-CGOp-bnr-g-04-0-UI.S1 NIH_BMAP_Ret4_S2 Mus UI-M-CGOp-bnr-g-04-0-UI 3', mRNA sequence. Br463964 Br463964 GI:11533147
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PCR PRIMETS
FORWARD: AGGADACAGCTATGACCAT
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Seq primer: ATTTAGGTGACACTATAG.
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  Eukaryota;
              Mus musculus
                           house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lb="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
152 c 149 g 129 t
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 Metazoa;
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Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 9.9e-17;
0; Mismatches 229
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Craniata;
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Vertebrata;
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 Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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1285 ctccctaagtctgtgctaggagccctgatcgctgtcaatctcaagaactccctcaagcaa 1344
                                                                                                                                                                                                                                                                                                                                            CTGCCCAAGGCCGTCCTGGCTGCTGTCATTATTGTGAACCTAAAGGGCATGATGAAGCAG 118
                                                                                                                                                                                                                                                                                                                                                                      ctcaccgacccctactacctgtggaggaaggagcaagctggactgttgcatctgggtagtg 1404
CCAGATACGGATATTTATAGAGACGTGGCAGAATACTCTGGGGCCCAAGGAGGTCCCGGGT
                                            atggacactgacatttatgtgaatcccaagacctataatagggcccaggatatccagggg 1584
                                                                                                                                        tccgtcctggtcgtggtcttccagactcagtttcgaaatggctatgcactggcccaggtc 1524
                                                                                                                                                                                                                                                                     agetteeteeteetteetteeteageetgeeetatggtgtggeagtgggtgtegeette 1464
                                                                                                                                                                                                                              ACCTTTGTGGCCACAATCCTGCTGAACCTGGACATTGGCCTGGCAGTTTCCATAGTCTTC
                                                                                                             TCCTTGCTGCTCGTGGTCCGAATGCAGCTGCCCCATTACTCCGTCCTGGGGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the retina tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 97044477
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Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Normalization and subtraction: two
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301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIF_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTCAGCGCGCAC"
a 124 c 120 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                various stages of development. For a detailed description of the library from which this clone was derived, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (Life Technologies)"
/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ultimately derived from mouse retina tissue libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UI-M-CGOp-bnr-g-04-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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59.0%;
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Pred. No. 1.8e-16;
0; Mismatches 146
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5' similar
BG727939
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
Www.genomesystems.com) (email contact: info@genomesystems.com) and
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Other_ESTs: fo79h02.x1
Contact: Stephen L. Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Genetics, Huntsville, Alabama (web address: ) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio
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Fax: 314 286 1810
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Site_2: XhoI; Oligo dT cDNA library constructed if
pooled from pooled kidney tissue from 300 adult
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/db_xref="taxon:7955"
/clone="4726491"
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                                                                                                                                                                                                                                          washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 6:
7el: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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vq35b04.rl Barstead bowel MI
IMAGE:1096207 5' similar to
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Mammalia; Eutheria;
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Location/Qualifiers
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                             /organism="Mus musculus"
/strain="FVB/N"
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Rodentia;
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/clone="IMAGE:1096207" /clone_lib="Barstead bowel

MPLRB9"

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Search completed: April 25, 2002, 13:42:26 Job time: 7981 sec
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Best Local Similarity 58.7%;
Matches 209; Conservative
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/dev_stage="8 weeks"
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    Query Match
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Sequence 1, Appli) <u> </u>	4 ω 6 '	Sequence 3, Appli Sequence 2, Appli	Sequence 3, Appli	Sequence 15, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 1, Appli	13	Sequence 15, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 13, Appl

ALIGNMENTS

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TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs
                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,045
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                            REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: PAPAS, Takis S.
MOLECULE TYPE:
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SOFTWARE: PatentI
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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RESULT 2
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APPLICANT:
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                           ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 TELECOMMUNICATION
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                           APPLICATION NUMBER: US/OFILING DATE: 11-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                    APPLICATION NUMBER: FILING DATE: 05-MAI
                                                                                                                                    CLASSIFICATION:
                                                                                                                                                APPLICATION NUMBER: US 0: FILING DATE: 17-APR-1995
               REFERENCE/DOCKET NUMBER:
                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                          CITY: Washington,
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3000 K Street, N.W.,
ashington, D.C.
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INFORMATION:
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Best Local Similarity 51.7%;
Matches 798; Conservative
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TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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                          GACAAACTTCCAGTGCCCATTCCAATCGAATTCATTATGACCGTGATTGCAGCAGGTGTA
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                                       ttcgctctcatcagcggtgccttcctggtgctggtgaaggagctcaatgctcgctacatg
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Pred. No. 1.4e-71
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US-09-184-937-1
; Sequence 1, Application US/09184937
; Patent No. 621087
; GENERAL INFORMATION:
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APPLICANT: PAPAS, Takis S
TITLE OF INVENTION: COlon
TITLE OF INVENTION: Expres
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                           3000 K Street, ashington, D.C.
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FEATURE:
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LOCATION:
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Best Local Similarity
Matches 798; Conserv
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMER: 29,768
REFERENCE/DOCKET NUMBER: 40399/354/NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 05-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,937
FILING DATE:
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TOPOLOGY: linear
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               agctatgtggacacagccatggaggctgagaggctgcacgtgtcagctacgctagcc 531
                                                                                                                                                                                                                                                                                      | Cagatggtgccaggtacctttgccgttatcagcatcctggtggg------taaca 412
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                                                                GTGCTTTCTGGAATCATCCAGTTGGCTTTTGGGATTCTGCGGATTGGATTTGTAGTGATA
                                                                                  tgcctcaccgccatccatccagatgggtctggggcttcatgcagttttggcttttgtggccatc 591
                                                                                                                                 AATAATTCTTCACTACTGGATGACGAGAGGGTGAGGGTGGCGGCGGCGCGCATCAGTCACA
                                                                                                                                                                                                    GCAGTTTCAAAAGCAGTCCCAGATCGCAATGCAACTACTTTGGGATTGCCTAACAACTCG
                                                                                                                                                                                                                       tctgtctgcagctggccccagagtcgaaattccaggtcttcaacaatgcc-accaatgag 471
                                                                                                                                                                                                                                                                     CACATATCCGTGGGTCCGTTTCCGATTCTGAGTATGATGGTGGGACTAGCAGTTTCAGGA 613
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DEDNESS: double
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185..2479
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	GGTTTCTTTAGGCGGAAACTTATC	1814	Db
	ctctactttgccaactcagagatcttcaggcaaaaggtcatcg 1654	1612	Qy
1813	TTATGATATGTATGAGCCAGAAGGAGTGAAAATTTTCAGATGTCCATCTCCT	1754	DЬ
1611	cctataatagggcccaggatatccaggggattaaaatcatcacgtactgctccct	1552	Qy
1753	Þ	1694	Db
1551	tatgtgaatccc	1492	Qy
1693	TCAGGACC	1634	Db
1491	tatggtgtggcagtgggtgtcgccttctccgtcctggtcgtggtcttccagact	1432	Qy
1633	GATTGTTTAATTTGGATCATGACCTTCATCTTCACCATTGTCCTGGGA	1574	ДЪ
1431	agcaagctggactgttgcatctgggtagtgagcttcctctcctccttcttcctcagc	1372	Qy
1573	GCATTGGGAAACTTAAAGGGAATGCTGATGCAGTTTGCTGAAATAGGCAGATTGTGGCGA	1514	Db
1371	ctactacctgtggagg	1312	Qy
1513	AAAAGTCCGTCCTGGCAGCTTTA	1454	Db
1311	accatgctggtcctggggatctatctgtatcctctccctaagtctgtgctaggagccctg	1252	Qy \
1453	GAGAGCACAGGAGGCAAAAACACAGATTGCTGGGCTTATTGGTGCCATCATCGTGCTGATT	1394	Db
1251		1192	Qy
1393	GTCTGTGGAGTATTCAGAGGATTTGCTGGGAGTACTGCCCTCTCCAGATCAGCAGTTCAG	1334	Db
1191	atgtcatttgctgtgcgctttctgtcactctggctgtg	1132	Qy
1333	GTAACATA	1274	Db
1131	cgctctcggctgcagcaacttc	1072	Qy
1273	GCTCTATTCCCTC	1214	Db
1071	tatgggccggaccctggccaac	1012	Qy
1213	GGATTTCAGCCCCCTATTACACCTGACGTGGAGACTTTCCAAAACACCCGTAGGAGATTGC	1154	Db
1011	caccccggtgtcgcctgtggtctcacagtggaaggacatgataggcacagcc	. 952	Qy
1153	Ç	1094	. Db
951	atccaacgc	892	Qy
1093	GACAAACTTCCAGTGCCCATTCCAATCGAATTCATTATGACCGTGATTGCAGCAGGTGTA	1034	Db
891	ttccccatccctacagagatgattgtggtggtggtggcaacagctatc	832	Qy
1033	TGATTGTCCTTTTGGTTGTATCCATTGTTAAAGAAATAAAT	974	Db
831	tcatcagcggtgccttcctggtgctggtgaaggagctcaatgctcgctacatg	772	Qy
973	TGTATTCTCACAAATAGAGAAGACTAATATTGCAGACCTGGTG	914	Db
771	tttaccttcattgacatttgcaaaaacctcccccacaccaacatcgcctcgctcatc	712	Оу
913	TCCCAACTCAAATTCATTTTTCAGTTGACAGTCCCGTCACACACTGATCCAGTTTCAATT	854	Db
711		652	Qy

RESULT 4 US-09-385-982-129 ; Sequence 129, Application US/09385982 ; Patent No. 6262334

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(588)
; OTHER INFORMATION: n = A
US-09-385-982-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 129
LENGTH: 588
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                                                                                         Sequence 513, Application US/09385982 Patent No. 6262334 GENERAL INFORMATION:
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Best I
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CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
                                 APPLICANT: ENDEGE, WILSON O., ET AL. TITLE OF INVENTION: NOVEL HUMAN GENETITLE OF INVENTION: PRODUCTS: II
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TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
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REFERENCE: CCDI
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Pred. No. 9.7e-21;
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; TYPE: DNA
; ORGANISH: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(623)
; OTHER INFORMATION: n = A
US-09-385-982-513
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US-09-385-982-146
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EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
Matches 258; Conserva
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Pred. No. 1.3e-18;
0; Mismatches 229;
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GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111

GENE

EXPRESSION

; Sequence 146, Application US/09385982 ; Patent No. 6262334

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RESULT 7
US-09-385-982-477
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; LOCATION: (1)...(475)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-146
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EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 146
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                  Sequence 477, Application US/09385982 Patent No. 6262334
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Best Local :
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                                                                                         CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
             EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
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ORGANISM: Homo :
FEATURE:
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Similarity 56.5%;
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Pred. No. 2.4e-17;
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GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXP
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/1098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SCOTTMARE: PASTSEQ for Windows Version 3.0
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; NAME/KEY: misc_feature
; LOCATION: (1)...(595)
; OTHER INFORMATION: n =
US-09-385-982-477
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                                                                                                                                                                                                                                                                                                                             Sequence 491, Application US/09385982 Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 261; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                SEQ ID NO 491
LENGTH: 583
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TYPE: DNA
ORGANISM: Homo
ORGANISM:
                   TYPE: DNA
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FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)...(583)
; OTHER INFORMATION: n = A,T,C
.US-09-385-982-491
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Best Local Similarity
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                                                                ATTURNET Stephen A.

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 3047

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)833-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
    INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1476 cgtggtcttccagactcagtttcgaaatggctatgcactggcccaggtcatggacactga 1535
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CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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RESULT 10
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; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07637865 Patent No. 5942427
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koyama, Yasuji
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Nakano, Elichi
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                                                                                                                                                                                                                     STREET: One Thomac CITY: Washington
APPLICATION NUMBER: JP 01-338267 FILING DATE: 28-DEC-1989
                                             CLASSIFICATION:
                                                        APPLICATION NUMBER: UFILING DATE: 19901227
                                                                                                                                                                                 ZIP:
                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                        Banner,
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2.7%; Pred. No. 0.000
ative 214; Mismatches
                                                                                                                                                                                                                                                                                                 N-Acetylmannosamine Dehydrogenase Gene and No. 5942427el Recombinant DNA as Well as a Met Productin of N-Acetylmannosamine Dehydrogenase
                                                                                                                                                                                                                                        Birch, McKie & Beckett
Circle, NW
                                                                      US/07/637,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.8; DB 1
No. 0.00063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-296-7830 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                  TITLE OF INVENTION: 1
TITLE OF INVENTION: 5
TITLE OF INVENTION: 6
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        tent No.
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LENGTH: 816 base pairs
TYPE: NUCLEIC ACID
            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 CCGGCAACAACACC 618
                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1..8
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                                                                                                                     COUNTRY:
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                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                       New York
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                                                                                                                                       New York
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                                                                                                                       U.S.A.
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                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                              Russo, James J.
                                                                                                                                                                                                                                                                                                                                            Chang,
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                                                                                                                                                                                                                  Encoding Same And Uses Thereof
                                                                                                                                                                                                                                               Sarcoma-Associated Herpesvirus,
                                                                                                                                                                                                                                                               Immediate Early Protein From Kaposi's
US/08/728,323A
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Pred. No. 0.0061;
0; Mismatches 91;
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Best Local Similarity
Matches 158; Conserv
                                                                                                                                                                                                                                                                                             Sequence 20, Appl Patent No. 584956
                                                                                                                                                                                                                                                                              GENERAL
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                               ADDRESSEE: Cooper & Dunham LLP
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                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                  NUMBER OF SEQUENCES:
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LOCATION:
                                    COUNTRY: U
ZIP: 10036
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CLASSIFICATION:
                                                                     STATE:
                                                                                   CITY: New York
                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                    New York
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                                                                                                   1185 Avenue of the Americas
                                                     U.S.A.
                                                                                                                                                                                              Edelman, Isidore
Moore, Patrick S.
                                                                                                                                                                                                                              Bohenzky, Roy A. Russo, James J.
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                                                                                                                                                               POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                               Isidore S.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                               TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 20
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                                                                                                                                                                    APPLICANT: Edelman, Isidore S. APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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                                                                                               CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
SOFTWARE: Patent:
                                             STREET: 1185 A
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/770,379
              COUNTRY:
                                STATE: New York
                                                                                 ADDRESSEE:
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10036
                                                                  1185 Avenue of
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              U.S.A
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SYSTEM: PC-DOS/MS-DOS
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                                                                                 Cooper & Dunham LLP
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Pred. No. 0.027;
0; Mismatches 183;
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                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                         Sequence 2 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                     SEQ ID NO 2
                                                           APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing of TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                        21009 CCTTATTGTCATTGTCATCCTTGTCAACCTGACTTTCCTTG 21049
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TOPOLOGY: line
MOLECULE TYPE: [
LENGTH: 1931
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
, REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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hes 158;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-130-114-2
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Best Local Similarity 46.4%;
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                           APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY_AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
                                                                                                                                 APPLICATION NUMBER: US/08
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 27709
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: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                 USA
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Knechtle, Philipp
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Steiner, Sabine
Mohr, Christine
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Pred. No. 0.021;
0; Mismatches 177;
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
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US-08-998-416-211
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Best Local Similarity
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ORIGINAL SOURCE:
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                          460
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nilarity 49.2%;
Conservative
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Pred. No. 0.036;
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Search completed: April 25, Job time: 9530 sec 2002, 14:39:50

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS1/gcgdata,
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

RESULT AAD00611 Human membrane transport protein, MTRP-12 cDNA. 29-AUG-2000 AAD00611 standard; cDNA; 2580 BP (first entry)

antithyroid; immunosuppressive; thyromimetic; antidiabetic; nootropic; antidiarrheic; neuroprotective; antidepressant; nephrotropic; virucide; antihelminthic; protozoacide; antibacterial; neuroleptic; antigout; diagnosis; prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzheimer's disease; depression; schizophrenia; immune disorder; allergy; inflammatory disorder; AIDS; Addison's disease; atherosclerosis; gout; Graves disease; Hashimoto's thyroiditis; microbial infection; cancer; cell proliferative disorder; ss. Human; membrane transport protein; MTRP-12; antiinflammatory; cytostatic;

Homo sapiens.

CDS 04-NOV-1999; 11-MAY-2000. WO200026245-A2 99WO-US26048 /product= " Location/Qualifiers 32..2308 "Membrane transport protein-12"

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treating, proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disease;
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          Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the
                                                                                                         ( HUMA - )
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DB; AAM42394.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAI62752-AAI62961) and (AAW42347-AAW423415) useful for preventing, treating or amelia medical conditions e.g. by protein or gene therapy. The generation of the process of the protein or generated from a condition of the process of the protein or generated from the protein or generat
                                                                                                                                    Human secreted
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                                                                                                                                    EST,
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; Pred. No. 8.5e 
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-of primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
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 AAQ71399;
                               AAQ71399 standard;
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Pred. No. 1.6e-74;
                             ВP
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2882 BP; 839 A; 579 C; 595 G; 868 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 21-25; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide that is down regulated in colon adenocarcinomas and adenomas - is used as an indicator of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-303023/37.
P-PSDB; AAR60568.
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n adenocarcinoma; diagnostic; therapeutic; ds.
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                                                                        cacatatccgtgggtccgtttccgattctgagtatgatggtgggactagcagtttcagga
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Query Match Best Local S Matches

cal Similarity 49.775; Conservative

10.7%; 49.3%;

Score 242.2; Pred. No. 2e

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Mismatches

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Gaps

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aaacttcgcaatgccttcagatgttcctcagccaagatcaaagctgtggtgttttgggctg.165

aagcttcagaagagttgccagtgtaatgcaaccaaaatcagaaataggatttttgatttt

ctgcctgtgctctcctggctccccaagtacaagattaaagactacatcattcctgacctg 225

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                     sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence encodes the rat DTDST protein used in the method of the invention.
                                                                                                                                                 This invention describes the construction of a novel vector for sulfate transporter expression containing a DNA sequence encoding a mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian
                                                                                                                                                                                                                                                Sulfate transporter gene expression vector
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/product= "DTDST"
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a

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30-JUN-2000;
03-AUG-2000;
                 The present invention relates to single exon nucleic acid probes (SEN The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders.
                                                                                                                                     WPI;
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genetic disorder; ;
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                                                                                                                                              The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                        Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fro
                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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Best Local Similarity 48.0%;
Matches 548; Conservative
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                The present invention relates to novel single exon nucleic acid profile present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the hybridises at high stringency to a nucleic acid expressed in the human straing, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory disease include: breast cancer, disorders of development, inflammatory disease of the breast fibrocystic changes, proliferative breast disease are non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the present of the properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25;
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                                                                                Sequence 1521
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                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndroms sinclude the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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            for receptor activity, arthritis and
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                                                                               Novel nucleic acids useful for treating
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Dwivedi P,
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99US-0117393
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Ford DM,
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                                                                             proteins for identifying therapeutic agents diagnosing cancer, especially colon cancer
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Claim 16;

Page

176; 345pp;

English

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human nucleotide sequence which

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                                       09-MAR-2000
                                                                                                                                                                                                                                                                                                    Human colon cancer differentially expressed nucleotide sequence #513.
                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2000
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ed. No. 2.8e-20;
Mismatches 225;
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Query Match Best Local

Similarity

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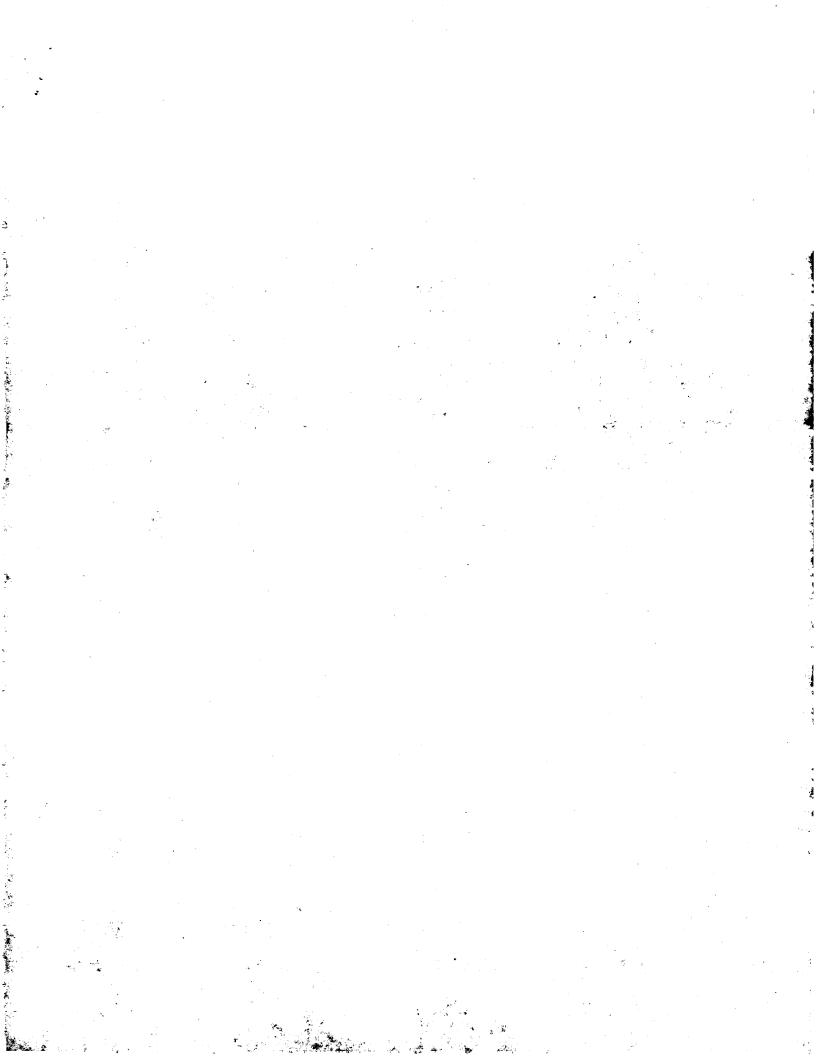
DB 21;

Length

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levels in normal cells. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence can also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of a cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also be cancer, preferably colon cancer. Antibodies against the protein encoded by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing colon cancer at an early stage.
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Catino TJ,
                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                             This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression
                                                                                                                                                                                                                                                                             Claim 16; Page 331-332; 345pp; English
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27-JAN-1999;
Sequence 623
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99US-0117393
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Ford DM, Lew
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ng cancer, especially colon o
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Search completed: April 25, 2002, 14:41:58 Job time: 6000 sec



Result No.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	RESULT 1 AF337809 LOCUS DEFINITION ACCESSION VERSION KEYWORDS			42 71.			3 G		31															389	١ (
Norway rat. Rattus norv Eukaryota; Mammalia; E Mattus. 1 (bases 1 Ye,H.J., Bi Molecular C (DRA) mRNA Unpublished 2 (bases 1 Ye,H.J., Bi	AF337809 Rattus no cds. AF337809 AF337809.		ω ω		υ ω ω ω	44	~ ~	88.	ω ω :	999	999	9 10.	2.2 10.7	112.	2 14. 9 12.	2 14.	14.	14.	14.	114.	15.	. w .	5 17. 1 16.	.4 17.	· • • • • • • • • • • • • • • • • • • •
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Submitted (17-JAN-2001) Section of Digestive Diseases, Yal
University School of Medicine, 333 Cedar Street-1080 LMP,
Haven, CT 06520-8019, USA
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IGRLWKKDKYDCLIWIMTFIFAIVLGLGLGLAASVAFQLLTIVFRTQFPKCSTLANVG
RSNIYKNKKANADVYEDEGVKIFRCDSTIYFANIGFFKGKIDAVGFNDLRILKKRNK
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                 TGCTCCCGTGCTCGGGCCTATGCCCTTCTGCTCCAACACCTCCCGGTTTTGGTCTGGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JUL-2000) Zentrum fuer Molekulare Neurobiologie, University of Hamburg, Falkenried 94, Hamburg 20251, Germany
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Waldegger, S., Jentsc
Direct Submission
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1 (bases 1 to 2889)
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AF279265.1 G
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Direct Submission
Submitted (16-JUN-2000) Finnish Genome Center, University
Helsinki, Tukholmankatu 2, Helsinki 00014, Finland
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LKOLOKEEKLRKOAASPKGASYSINVNTSLEDWRSNNVEGCKMTOV
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801 c 785 g 610 t
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Mus muscu
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                                                                                                                                                          Submitted (23-MAR-1999) Center
                                                                                                                                                                                                                                                                           Melvin,J.E., Park,K., Richardson,L., Schultheis,P.J. and Shull,G. Mouse down-regulated in adenoma (DRA) is an intestinal
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                            Mus musculus
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AF136751.1
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                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                           house mouse
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131. .2404
/gene="Dra"
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                                    /tissue_type="colon"
/dev_stage="adult"
1. .2629
                                                                                     /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                     Location/Qualifiers
                                                                                                              /organism="Mus musculus"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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Direct Submission
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Submitted (20-ApR-2001) Internal Medicine, Yai
333 Cedar Street, P.O. Box 208029, New Haven,
Location/Qualifiers
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Mammalla; Eutheria; Rodentia; Sciut
1 (bases 1 to 2612)
Knauf, F., Yang, C.L., Thomson, R.B.,
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AY032863
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                  DLLIWLVTFVATILLNLDIGLAVSIVESLLLVVVRMQLPHYSVLGQVPDTDIYRDVAE
YSGAKEVPGVKVFRSSATLYRANAELKSDSLKEKCGVDVDRLLTOKKKEKKOEMKLK
RMKKAKKSQKQDASSKISSVSVNVTTULEDVKSNDVEGSEAKVHQGEELDDVVSSNQE
DAKAPTMTSLKSIGLPQPGFHSLILDLSTLSFVDTVCIKSLKNIFRDEFREIEVEVYIA
ACYSPVVAQLEAGHFFDESITKQHVFASVHDAVTFALSHRKSVPKSPVLATKL"
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Everett, L.A. and Gre
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/protein_id="AAD51618.1"
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                                           Direct Submission
Submitted (09-JUL-1999)
                                                                          Everett, L.A.
                                                                                                         99380587
               National Institutes of MD 20892-4431, USA
                                                                                                                                                                Everett, L.A., Morsli, H., Wu, D.K. and Green, E.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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GTACTTGGCAGACCCCTTGGTTGGCGGATTCACAACCGCTGCAGCCTTCCAAGTACTGGT
                                                                                      TCTTCTAGTTGGAATCATACAGCTGGTGTTTGGAGGTTTGCAGATTGGATTCATAGTGAG
                                                                                                                                                                          GAGCATGGCTCCAGATGACCACTTTCTTGTGCCCAGCGGTAACGGAAGTGCATTGAACTC 734
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LTIIVCMAVKELNDFFKHRIPVPIPIEVIVTIIATAISYGANLEKNYNAGIVKSIPSG
FLPPULPSVGLESDMLAASESIAVVAYAIAVSYGKVYATKHDYVIDGRQEFIRFGISU
VFSGFFSCFVATTALSRTAVQESTGGKTQVAGLISAVIVMVAIVALGRLLEPLQKSVL
AAVVIANLKGHFMQVCDVPLMKQNKTDAVIWVFCINSIILGDLGLLAGLLEFALLT
VVLRVQFPSMROLGSVBSTDIYKSITHYKNLEEPEGVKILRFESSPIFYGNVDGFKKCI
VSTYQFDAIRVYNKRLKALRRIQKLIKKGQLRATKNGIISDIGSSNNAFEPDEDVEEP
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/strain="BALB/c"
/db_xref="taxon:10090"
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Pred. No. 1.2e-61;
0; Mismatches 741;
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RESULT AY024359 LOCUS DEFINITION

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AY024359 Mus musculus

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ROD

17-JUL-2001

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Best Local Similarity
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AAGGACAAAGTCACAGAGTCCATTGGAGATAAGCTGAAGCAGGCATTCACGTGTACTCCT 162
                                                                                                      CTTCCCCAAGGCTTAGCCTTCGCCATGCTGGCAGCCGTGCCTCCGGTGTTTGGCCTGTAC
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Submitted (25-JAN-2001) NIDCD, NIH, Bl
Drive, Bethesda, MD 20892-4163, USA
On Jul 17, 2001 this sequence version
Location/Qualifiers
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Adler, H.J., Merritt, R.C.
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1 (bases 1 to 2235)
Adler, H.J., Merrittt, R.C. Jr., Belyantseva, T.A.
Mus musculus organ of Corti mRNA for prestin
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Eukaryota; Metazoa;
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AY024359.2
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="prestin"
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VVNDLTRNNFFENPALKELLFHSIHDAVLGSQVREAMAEQEATASLPQEDMEPNATPT
TPEA"
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/db_xref="taxon:10090"
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Pred. No. 3.5e-61;
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Characterization of rat and rabbit brush border
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Location/Qualifiers
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/protein_id="AAKO0897.1"
/db_xref="Gi:12656494"
/translation="FPIASWLPEYKLKEWLLSDIVSGISTGLVAVLQGLAFALLVNIP
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DDSLTNKRIMVAASVTFLTGGIQLAFGILRIGFFVIYLSEALISAFTTAAALHVVISQ
LKFMLQLTVPAHTOPFSIFKVLESLFTQIRKTNIADLVTGRVILVVIVFVFKEINERF
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EIGRLWKKDKYDCLIWIMTFIFAIVLGLGLGLAASVAFELLTIVFRTQFPKCTTLANI
GRSNIYKNRKDYS"
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/db_xref="taxon:9986"
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Gregor, M. and Seidler, U.
Characterization of rat and
exchange and DRA expression
Unpublished
                                                                                                                                     Rossmann,H., Jacob,P. and Seidler,U.
Direct Submission
Submitted (16-OCT-2000) Abteilung Innere Medizin I,
Tuebingen, Otfried Mueller-Str. 10, Tuebingen 72076,
Location/Qualifiers
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Mammalia; Eutheria;
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                           /gene="Slc26a3"
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/strain="Wistar rat"
/db_xref="taxon:10116"
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Murinae;
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                                                                    GTGACTGTTCTTGGGAATCATTCAGTTGCTCCTGGGGGGTTCTGCAGATAGGCTTTGTG
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LTIVFRYQFPKCSTLANVGRSNIYKNKKNYADVYEPEGVKIFRCPSPIYFANIGFFKQ
KLIDAVGFNPLRILRKRNKALKKIRKLQKQGLIQVTPKGFICTSDGFKDSDEELDNNQ
IEELDQPINTTDLPFEIDWNADLPLNITIPKISLHSL*
4 401 c 382 g 434 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                   14.78;
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Pred. No. 3.8e-60;
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Submitted (21-OCT-1997) Genome Technology Branch, Genome Research Institute, National Institutes of Convent Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Eutheria; Primates; Catarrhini; Homini
1 (bases 1 to 4930)
Everett,L.A., Glaser,B., Beck,J.C., Idol,J.R., F
Adawi,F., Hazani,E., Nassir,E., Baxevanis,A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                    1372
                                            Green, E.D.
Direct Submission
                                                                                  Everett, L.A.,
                                                                                                                             transporter gene
Nature Genet. 17
                                                                                                                                                      Green, E.D.
Pendred syndrome is caused by
                                                                      Adawi, F., Hazani, E.,
                                                                                                                 98061089
                                                                                                                                                                                                                                                         Homo sapiens
                                                        Ublus

Mases 1 to 4930)

Perett, L.A., Glaser, B., Beck, J.C., Idol, J.R.,

Perett, L.A., Glaser, B., Baxevanis, A.D.,
                                                                                                                                                                                                                                                                                                  GI:2654004
                                                                                                                                                                                                                                                                                                                          4930 bp
pendrin
                                                                                                                             (4),
                                                                                                                                          (PDS)
                                                                                                                                                                                                                                                                                                                              (PDS)
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                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                         mutations
                                                                                                                             (1997)
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                                                                      Buchs, A.,
Sheffiel
                                                                                                                                                                                   Buchs, A., Heyman, M. Sheffield, V.S. and
                 National Human
Health, 49
                                                                                                                                                                                                                                                                                                                                           01-DEC-1997
                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                         sulphate
                                                                      Heyman, M.
1, V.S. and
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tgcagtttggctttgtggccatctacctctccgagtccttcatccggggcttcatgacgg 628
                                                                                              tgcacgtgtcaggtaacgctagcctgcctcaccgccatcatccagatgggtctgggcttca 568
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/product="pendrin"
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/db_xref="g1:2654005"
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/translation="maapggrspppqlpeyScsymysrpvyselafqqoherrloek
mayallaavpvgyglysaffplltyfflegtsrhisvgpfpvyslmyggyltantlog
Mayallaavpvgyglysaffplltyfriggtsrhisvgpfpvyslmyggvliapp
LVgggrtaarpqvlysglkivlnvsytknyngtlsiiytlveifqohigfplyryladp
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LTIVVCMAVKELMDFFRHKIPVPPIPIEVITTIATAISYGANLEKNYNAGIVKSIPRG
FLPPELPPVSLFSEMLAASFSIAVVAYAIAVSYGKVAAFKYDYTIDAQQFLAFGISH
IFSGFFSCFVATTALSRTAVQESTGGKTQVAGIISAAIVMIAILALGKLLEPLQKSVL
AAVVIANLKGMEMQLCDIPRLMRONKIDAVIMVFTCIVSIIGLGULEFLQKSVL
AAVVIANLKGSEJFSTDIYKSTKNYKNIEEPQGVKILRESSPITYGNVDGFKKCI
KSTVGFDAIRVYNKRLKALRKIQKLIKSGQLRATKNGIISDAVSTNNAFEPDEDIEDL
EELDIPTKEIELQVDMNSELPVKNVBRVPIHSLVLDCGAISFLDVGVRSLRVIVKE
FQRIDVNYFASLQDYVIEKLEQCGFFDDNIRKOTFFLTVHDAILYLQNQVKSQEGQG
SILETITLIODCKDTLELIETELTEEELDVQDEAMRTLAS"

54 a 937 c 1082 g 1457 t
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1. .4930
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/db_xref="taxon:9606"
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TCAAGTCCA
                                tcatcgcca
                                                               AGATTCTTAGATTTTCCAGTCCTATTTTCTATGGCAATGTCGATGGTTTTAAAAAATGTA
                                                                                                                                    GCACAGATATCTACAAAAGTACCAAGAATTACAAAAACATTGAAGAACCTCAAGGAGTGA
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                                                                                                                                                                                                       TGTTGACTGTGGTCCTGAGAGTTCAGTTTCCTTCGTTGGAATGGCCTTGGAAGCATCCCTA
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                                                                                                               ctccccaagtacaagattaaagactacattcattcctgacctgctcggtggactcagcggg
TATGGGTTGTATGCATCCTTTTTCCCAGCCATAATCTACCTTTTCTTCGGCACTTCCAGA
                                                             ggatccatccaggtcccacaaggcatggccatttgctctgctggccaaccttcctgcagtc
                                                 GGGATTGTGGCCGTACTACAAGGTTTAGCATTTGCTCTGCTGGTCGACATTCCCCCAGTC
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Schweinfest, C.W., Henderson, K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon mucosa-associated Homo sapiens colon cDNA
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L02785.1 GI:291963
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                                                                                                                                                                                                  Similarity 51. 38; Conservative
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IDFTINTNGGLRNRYYEVPVETKF"
1 578 c 596 g 868 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Nuclear 1 579-583; acidic motif 653-676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA58443.1"
/db_xref="GI:291964"
                                                                                                                                                                                                                                                                                                                 LPFHIDWNDDLPLNIEVPKISLHSLILDFSAVSFLDVSSVRGLKSILQEFIRIKVDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DRA"
185. .2479
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/db_xref="taxon:9606"
/cell_type="epithelial cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DRA"
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Weintraub,L.A., Mohr-Tidwell,R.M., Pel
Leckie,M.P. and Green,E.D.
A collection of 1814 human chromosome
Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                             Email: egreen@nhgri.nih.gov
primer A: TCACCACATAGTTGCAAAGG
Primer B: GCATTTGTAGAATACACTGG
STS size: 113
PCR Profile:
                                                                                                                                                                                                                                                                     Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr. MSC4431, Bldg. 49, Rm. 2A08,
                                           Buffer:
                                                                                                                                                                                                                                                   Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                            Synonyms: DRA
GDB: GDB:3754367
                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                             Human chromosome
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Green, E.D.
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1 (bases 1 to 2881)
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Annealing:
Polymerization:
PCR Cycles:
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KCl:
           Tris-HCl:
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                                                                  TTCAAAGTACTATACTCTGTATTCTCACAAATAGAGAAGACTAATATTGCAGACCTGGTG
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51.7%; Pred. No. 7.2e
tive 0; Mismatches
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			_	agacctataatagggcccaggatatccaggggattaaaaatcatcacgtactgctcccct	AATTTCCAAAATGCAGCACGCTGGCTAATATTGGAAGAACCAACATCTATAAGAATAAA	agtttcgaaatggctatgcactggcccaggtcatggacactgacatttatgtgaatccc										atggagctggaggaaaatcccaggtggccagcctgtgtgtg						tctccctagccatcgtgagctacgtcatcaacctggctatgggccggaccctggccaac	GATTTCAGCCCCTATTACACCTGACGTGGAGACTTTCCAAAACACCGTAGGAGATTGC	ggttccccaccccggtgtcgcctgtggtctcacagtggaaggacatgataggcacagcc				

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1242.5.5
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Ogbash homo sapien
Ogbash homo sapien
Ogepho rattus norv
Ogjkq2 meriones un
Og9nh7 mus musculu
Ogr154 rattus norv
Ogweel mus musculu
Ogr154 rattus norv
Ogweel mus musculu
Ogrjy3 ovis aries
Oggjy3 ovis aries
Oggjy4 oryttolagus
Ogpd9 rattus norv
Oghzb4 homo sapien
Ogweel drosophila
Ozytosophila
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Q9erc6 rattus norv
)19447 caenorhabdi
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683	657	657	646	656	649	649	660	653	646	656	660	809	662	703	658	658	631	631	380	658	677	685	685	660	750
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Q9lm44 arabidopsis	Q9fpq4 solanum tub		004289 arabidopsis					Q91w86 arabidopsis		Q9at47 lycopersico	Q43482 hordeum vul	045016 caenorhabdi			Q9sv13 arabidopsis		Q9sxs2 arabidopsis	O49307 arabidopsis	a	Q9at12 zea mays (m					Q9sev7 guillardia

ALIGNMENTS

Qy	Db .	0ν	Db	Qγ	Query Best Match	SQ	DR	DR	DR	DR	DR	RL	RT	RT	RT	RA	RA	RP	RN	o x	8	8	SO	DE	DΤ	DT	DΤ	AC	ID	Q9NQU1	RESULT	
152 NNATNESYVDTAAMEAERLHVSATLACLTAIIOMGLGFMQFGFVAIYLSESFIRGFMTAA 211 : : : : : : : : :		92 FALLANLPAVNGLYSSFFPLLTYFFLGGVHOMVPGTFAVISILVGNICLOLAPESKFOVF 151	30 PRTHOMRTWLOCSRARAYALLLOHLPVLVWLPRYPVRDWLLGDLLSGLSVAIMQLPQGLA 89	6,1	Query Match 32.5%; Score 1258; DB 4; Length 738; Best Local Similarity 36.6%; Pred. No. 9.8e-71; Matches 261; Conservative 162; Mismatches 238; Indels 52; Gaps	SEQUENCE 738 AA; 80910 MW; 21DD30EF91AD3AA8 CRC64;	00916; Sulfate_transp; 1.	Pfam; PF01740; STAS; 1.	InterPro; IPR001902; Sulfate_transp.		EMBL; AF279265; AAF81911.1;	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	exchanger.";	characterization of PAT1, a candidate gene for pancreatic anion	ication of six putative anion		Lohi H., Kujala M., Kerkela E., Saarialho-Kere U., Kestila M.,	SEQUENCE FROM N.A.	[1]		Catarrhini; Hominidae	etazoa; Chordata;	Homo sapiens (Human).	ION TRANSPORTER 1.	(TrEMBLrel. 17,	(TrEMBLrel. 15,	2000 (TrEMBLrel.	Q9NQUI;	Q9NQU1 PRELIMINARY; PRT; 738 AA.	U1	LT 1 .	

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Best Local Sim
Matches 261;
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Carrier 26 Gene Family ";
Genomics 72:43-50(2001).
EMBL; AF288410; AAK19153.1;
SEQUENCE 759 AA; 82966 M
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SOLUTE CARRIER FAMILY 26 MEMBER 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                             Score 1258; DB 4;
Pred. No. 1e-70;
2; Mismatches 238;
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"The reciprocal electromechanical properties of molecule of rat outer hair cells."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ dEMBL; AJ303372; CAC21555.1; -. InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; 1.
Pfam; PF01740; STAS; 1.
SEQUENCE 744 AA; 81278 MW; E49E842CF7A3CD58
                                                                                                                                                                                                                                                                              Q9EPHO;
                                                                                                                                                                 Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                          SEQUENCE FROM N.A.
Ludwig J., Oliver D., Frank G.,
                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Last sequence update)
Last annotation update)
                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                            PRT;
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E49E842CF7A3CD58 CRC64
                                                                                                                            Kloecker N.,
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of rat
                                                                                     databases
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: Prestin:
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; Murinae; Rat
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Query Match
32.5%; Score 1255.5; DB 11; Length 744;
Best Local Similarity 35.4%; Pred. No. 1.4e-70;
Matches 265; Conservative 163; Mismatches 267; Indels 53; Gaps 11;

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Q9JKQ2;
Q9JKQ2;
01-OCT-2000
01-OCT-2000
01-JUN-2001
PRESTIN.
SEQUENCE FROM N.A.

MEDLINE-20279283; PubMed=10821263;
Zheng J., Shen W., He D.Z.Z., Long
"Prestin is the motor protein of co
                                                                                                             Meriones unguiculatus (Mongolian jird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Meriones.
                                                                                            NCBI_TaxID=10047;
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(TrEMBLrel. 15, Last sequence up
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EMBE; AF230376; AAF71715.1; -.

InterPro; IPR002645; STAS.

InterPro; IPR001902; Sulfate_tra
Pfam; PF00740; STAS; 1.

Pfam; PF00916; Sulfate_transp; 1
SEQUENCE 744 AA; 81418 MW; 1
Q99NH7;
Q99NH7;
01-JUN-2001
01-JUN-2001
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KFKEYVLGDLVSGISTGVLQLPQGLAFAMLAAVPPVFGLYSSFYPVIMYCFFGTSRHISI 134
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                                                                                                                                                                                        TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAK
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                                                                                                                                                                             MVKEYGDVGIYVYLAGCSPQVVNDLTRNRFFENPALK-ELLFHSIHDAVL----
                                                                                                                                                                                                                                 ATKPEEEDDEVKYPPIVIKTT-FPEELQRFMPQTENVHTIILDFTQVNFIDSVGVKTLAV
                                                                                                                                                                                                                                                                                                              FANSEIFRQKVIAKT------VSLQELQQDFENAPPTDPNNNQTPANGTSVSYI
                                                                                                                                                                                                                                                                                                                                         YGLTTAVIIALLTVIYRTQSPSYKVLGQLPDTDVYIDIDAYEEVKEIPGIKIFQINAPIY
                                                                                                                                                 PGHNFQGAPGDAELSLYDSEEDI
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Sulfate_transp.
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, Created)
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Best Local Similarity 36.8
Matches 262; Conservative
Q9R155;
Q9R155;
Q1-MAY-2000
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=ORGAN OF CORTI;
STRAIN=C57BL/6; TISSUE=ORGAN OF CORTI;
Adler H.J., Merritt R.C. Jr., Belyantseva I.A.,
"Mus musculus organ of Corti mRNA for prestin.",
"Mus musculus organ of Corti mRNA for prestin.",
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ da
EMBL; AY024359; AAG59999.1; -
SEQUENCE 744 AA; 81380 MW; 56E842748288E96F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
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                                                                                                       VDGENATKPEEEDDEVKFPPIVIKTT-FPEELQRFLPQGENVHTVILDFTQVNFVDSVGV
 (TrEMBLrel. 13,
                    PRELIMINARY;
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36.5%; Pred. No. 9.90
Live 154; Mismatches
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MEDLINE-99380587; PubMed-10449762;
Everett L.A., Morsli H., Wu D.K., Green E.D.;
"Expression Pattern of the Mouse Ortholog of the Pendi
(Pds) Suggests a Key Role for Pendrin in the Inner Ear
Proc. Natl. Acad. Sci. U.S.A. 96:9727-9732(1999).
EMBL; AP167411; AAD51617.1; .

EMBL; AP167411; AAD51617.1; .

MOD; MGI:1346029; S1C2644.
R InterPro; IPR001902; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF001740; STAS; 1.
R Pfam; PF0016; Sulfate_transp: 1.
R Pfam; PF00916; Sulfate_transp: 1.
R Pfam; PF00916; Sulfate_transp: 1.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                      GVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYF
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                                               TFSPDSSSPAQSEPPASAEAPGE----PSDMLASVP----PFVTFHTLILDMSGVSFVD
                                                                                                                                                                                     YDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITML | :| | | | | | | :::||: ::
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Metazoa; Chordata; C

Metazoa; Rodentia; S
                                                                                              KCINSTVGFDAIRVYNKRLKALRRIQKLIKKGQLRATKNGIISDIGSSNN--
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17,
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L%; Pred. No. 3.8e-66;
147; Mismatches 297
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RESULT
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01-MAY-2000
01-JUN-2001
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Q9R154;
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EMBL; AF167412; AAD51618 1; -
InterPro; IPR001902; Sulfate_transp.
InterPro; IPR002645; STAS.
Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
SEQUENCE 780 AA; 85714 MW; DAOCDB7496B8D535 CRC64;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99380587; PubMed=10449762; Everett L.A., Morsli H., Wu D.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENDRIN.
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                                                                                                                                                                                                                                                                                                                            LPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGVRSLRMIVKEFQRIDVNVYFALLQDDVLEKMEQCGFFDD-NIRKDRFFLTVHDAILH
GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK
                                                                                                                                                               FTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAIS 298
                                                                                                                                                                                                    LVGIIQLVFGGLQIGFIVRYLADPLVGGFTTAAAFQVLVSQLKIVLNVSTKNYNGVLSII
                                                                                                                                                                                                                                                                       YAVSRPVYSELAFQ----QQRERRLPERRTLRDSLARSCSCSRKRA--FGALKALLPILDW 74
                                                                                                                                                                                                                                                                                                                                                                                          YVVDRAAYSLTLEDDEFEKKDRTYPVGEKLRN--AFRCSSAKIKAVVFG----LLPVLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQNQVKS------REGQDSLLETVARIRDCKDPLDLMEAEM-----NAEEL
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                                       HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT
                                                                                                                                               YTLIEIFQNIGDTNIADFIAGLLTIIVCMAVKELNDRFKHKIPVPIPIEVIVTIIATAIS
                                                                                                                                                                                                                             LTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV 238
                                                                                                                                                                                                                                                         HISVGPFPVVSLMVGSVVLSMAPDDHFLVPSGNGSTLNTTTLDTGTRDAARVLLASTLTL
                                                                                                                                                                                                                                                                                                             LPKYRVKEWLLSDIISGVSTGLVGTLQGMAYALLAAVPVQYGLYSAFFPILTYFVFGTSR
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                                                                                            YGANLEANYNAGIVKSIPSGFLPPVLPSVGLFSDMLAASFSIAVVAYAIAVSVGKVYATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13,
(TrEMBLrel. 13,
(TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       143;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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.4e-66;
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QUENCE CONTROL OF CONT
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DOWN-REGULATED IN ADENOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FACE ..... SEQUENCE FACE .... SCHULTHEIS P.J., Shull G.E. STRAIN-FVE/N; TISSUE-COLON; Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E. Melvin J.E., Park K., Richardson L.A., Schultheis P.J., Shull G.E., Park K., Richardson L.A., Park K., Richar
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InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
SEQUENCE 757 AA; 83589 MW; 32B1AC648BE74A07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9WVC8
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Exchanger.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYVVDRAAYSLTLEDDEEEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65
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                                                                                                                                                                                                GTFAVISILVGNICLQLA--PESKFQVFNNAT-NESYVDTAAMEAERLHVSATLACLTAI 182
                                                                                                                                                                                                                                                                                                                                                           KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYVVARPVYSTKTFGEEFKKTHRHHKTFLDHLKGCCSCSSQKAKKIALSLFPIASWLPAY 67
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                                        GPFPVLSMMVGVVVTRVVSDPNASSELSSSSTENDSFIE----
                                                                                                                                                                                                                                                                                                                      KIKEWLLSDIVSGISTGLVAVLQGLAFALLVNIPPAYGLYAAFFPVITYFFLGTSRHISV 127
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IQLLLGVLQVGFVVIYLSESLISGFTTAAAIHVLVSQLKFMLQLPVPAYSDPFSIFKVLE
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34.78;
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Pred. No. 8.2e-
49; Mismatches
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Best Local S
Matches 231
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DTD SULFATE TRANSPORTER.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Baumgartner B.G., Kriegesmann B., Brenig B.;

"Cloning and characterization of the bovine DTD sulfate (bDTDST) gene.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ232615; CAB69640.1;

SEQUENCE 734 AA; 81540 MW; D5224A27EA5D691E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                     SIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQL 142
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ILLVPQSIAYSLLAGQEPIYGLYTSFFASLIYFILGTSRHISVGIFGILCLMIGEVVDRE
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32.8%;
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Pred. No. 1.2e
17; Mismatches
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Kriegesmann B., Baumgartner B.G., Deppe A., Brenig B.;
"Sequence of the ovine sulfate transporter gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18558; CAC20729.1;
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Ffam; PF001740; STAS; 1.
Pfam; PF001740; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyia; Ruminantia; Pecora; Bovoidea Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, SULFATE TRANSPORTER.
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                                                                                                                                                        SEQUENCE FROM N.A.
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Query Match Best Local Sim Matches 229;

Similarity

25.9**%**; 33.2**%**; 132;

Score 1001.5; DB Pred. No. 1.1e-54; 32; Mismatches 281

281; 6;

Indels Length

47;

Gaps

8

Conservative

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RESULT 11
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Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-JUN-REGULATED IN ADENOMA DE
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                                               "Characterization of rat and rabbit brush border membrane exchange and DRA expression in rabbit, rat, and human ducc Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF314819; AAK00897.1; •.
                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
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                                                                                                                                               Jacob P., Rossmann H., Lamprecht
Gregor M., Seidler U.;
                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-INTESTINAL MUCOSA;
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a; Leporidae; Oryctola;
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NON_TER 1 1 1
NON_TER 545 545
SEQUENCE 545 AA; 59322 MV
                                                                                                                                                                                                                                                                                                                        Jacob P., Rossmann H., Lamprecht G., Kretz A., Neff C., Li
Gregor M., Seidler U.;
"Characterization of rat and rabbit brush border membrane
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-WISTAR RAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOWN-REGULATED SLC26A3.
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183; Conser
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Conservative 10
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(TrEMBLrel. 17, Last annotation updat
                                                                    Conservative
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Pred. No. 1.6e
D5; Mismatches
                                                               Score 882.5; DB 11;
Pred. No. 2e-47;
4; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                               Query Match
Best Local (
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Genomics 70:102-112(2000).

Genomics 70:102-112(2000).

EMBL; AF297659; AAG22075.1; -

InterPro; IPR003880; Phosphopant_attach.

InterPro; IPR001902; Sulfate_transp.

InterPro; IPR001902; Sulfate_transp.

Pfam; PF001740; STAS; 1.

Pfam; PF00916; Sulfate_transp; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

SEQUENCE 701 AA; 74991 MW; F37DC87F6A036676 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loh1 H.,
Kere J.;
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SULFATE/ANION TRANSPORTER SAT-1 PROTEIN.
SLC26A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mapping of Five New Characterization of 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE-20541715; PubMed-11087667;
Lohi H., Kujala M., Kerkela E., Saarialho-Kere U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H2B4
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| KNYADVYEPEGVKIFRCPSPIYFANIGFFKQKLI 453
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                                                                                          RTYPVGEKLRNAFR-----
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                                                 RQRPAPRGLREMLKARLWCSCSCSVLCVRALVQDLLPATRWLRQYRPREYLAGDVMSGLV
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                                                                                                                                                               Similarity
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC26A6,
                                                                                                                                                            29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative
                                                                                                                                         146;
                                                                           -CSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLS
                                                                                                                                                            Score 878; DB 4;
Pred. No. 5.2e-47;
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\ Candidate Gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                       Mismatches
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                                                                                                                                         304;
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                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes
                                                                                                                                                                                  Length 701;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kestila
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atic Anion
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                                                                                                                                       Gaps
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Q9VVM6;
Q9VVM6;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-JUN-2001 (TrEMBLrel. 17, L
CG5485 PROTEIN.
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell G., Nelson C.R., Miklos G.L.G.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAGDIPTGFMPPQVPEPRLMQRVALDAVALALVAAAFSISLAEMFARSHGYSVRANQELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANVCDVVTSTVCLAVLLAAKELSDRYRHRLRVPLPTELLVIVVATLVSHFGQLHKRFGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFGFVAIYLSESFIRGFWTAAGLQILISVLKYIFGLTIPSYTGFGSIVFTFIDICKNLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILSRGGFLGEGPGDTAEEEQLFLSVHDAVQTARARHRELEATDAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLAGRTQRPRTALLARIGDTAFYEDATEFEGLVPEPGVRVFRFGGPLYYANKDFFLQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVGEIORGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELQLAGFDPSQDGLQPGANSSTLNGSAAMLDCGRDCYAIRVATALTLMTGLYQVLMGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAKTYSLQELQQDFENAPPTDPNNNQTPANGTSVSYTTFSPDSSSPAQSEPPASAEAPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSVLACVIVVSLRGALRKVWGFPRLWRMSPADALVWAGTAATCMLVSTEAGLLAGVILSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVGCCNVLPAFLHCFATSAALAKSLVKTATGCRTQLSSVVSATVVLLVLLALAPLFHDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLGFVSAYLSQPLLDGFAMGASVTILTSQLKHLLGVRIPRHQGPGMVVLTWLSLLRGAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LQLA--PESKFQVFNNATNESYVDTAAM-----EAERLHVSATLACLTAIIQMGLGFM
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                              Brachycera; Muscomorpha,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Meikulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelliams S.M., Myers E.W., Rubin G.M., Venter I., Sang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
Pine genome sequence of Drosophila melanogaster.*;
DR EMBL; AE003522; AAR49285.1;
DR InterPro: IPR001902; Sulfate_transp.

DR Fighas; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 210; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; SEQUENCE 742 AA; 80315 MW;
      442
                                             443
                                                                                                                            383
                                                                                                                                                                     322
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                                                                                                                                                                                                                                                                                                                                                                          LKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVN 441
                                                                                                                     PVLPRLDLVPKVAVDSIAIAIVTYSIIMSMGLTFAKKHGYEVRPNQELFAMGIGNMVGGC 442
                                                                                                                                                 PVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSF
                                                                                                                                                                                                                              GAFLVLVKE-LNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPT
                                                                                                                                                                                                                                                                                          LVNGFTTAAACHVVTAQLKDVLGISVPRHKGAFKIIYTVIDVIKGVPQTNLVNFGFCMAV
                                          FSCIPMACSLSRSVIQDQTGGVSQIASLVSASLVVVTLMWIGPFFSSLPRCVLAGVIIVA
                                                                                                                                                                                                       IAFMMICNEILKPRLSKKCRFPLPAELIMVIGGTLISKWFNLYVDYNVNPVGKIPSGLPE
                                                                                                                                                                                                                                                                                                                               FIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTSKHISIGTFAVASMMTAKVVDTYANVDDHHQILPINAFGLQSNGTATASPLLLINSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGVHQMVPGTFAVISILVGNIC------LQLAPESKFQVFNNAT------NES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKPKIQPKYSIHRDVLTHEVVIKQTGYAARDKSIP--SSLRNCWR--SWNFFALFTGVIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILQWLPQYSPRRDLPGDIIAGFTVAIMNIPHGMAYGILAGVSAGNGLYMAVFPVLAYMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.0%; Score 852; DB 5; Length 7/ 11arity 28.3%; Pred. No. 2.4e-45; Conservative 158; Mismatches 301; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 ----AAMEAE----RLHVSATLACLTAIIQMGLGFMQFGFVAIYLSES
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E68FC76976312207 CRC64
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                    Pfam; PF00916; Sulfate_transp; Pfam; PF01740; STAS; 1.
SEQUENCE 611 AA; 67595 MW;
                                                                                                                                                                                                                                                                                                               "2.2 Mb of contiguous nucleotide sequence from chromosome elegans.";
                                                                                                                                                                                                                                                                                                                                          Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke Smaldon N., Smith A., Sonnhammer E., Stadden R., Sullston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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Caenorhabditis elegans.
Chromadorea;
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EMBL; 270757; CAA94798.
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Rhabditidae; Pelode
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InterPro; IPR002645; STAS.
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                                                                                TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLG 77
GLTVGIMHVPQGMAYASLAGVPPVYGMXSSFFASTIYMFFGTARHISIGVFAVASMMVGA 113
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Pred. No. 5.1e-41;
8; Mismatches 262
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ISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDV 706	SDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYND 671	AKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEP	VVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDI-QGIKIITYCSDLYFANSEIFRQKVI : : : : : :	VLGALIAVNLKNSLKOLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLV 492 : :: :	GCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKS 432	GEIORGEPTDVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIAL 372	FALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIV 312 	YLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLI 257 -	138 ICLQLAPESKFQVFNNATNESYYDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAI 197
	71 78	611 518	551 511	92	32 07	72	12 87	57 31	97

Search completed: April 26, 2002, 09:06:43 Job time: 134 sec

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OM protein - protein search, using sw model
April 26, 2002, 09:04:39; Search time 12.77 Seconds (without alignments) 2161.990 Million cell updates/sec
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Title:
Perfect score:
Sequence: US-09-749-589-2 3869 1 MSQPRPRYYVDRAAYSLTLFWDLEQEMFGSMFHAETLTAL 753

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 100059

100059 seqs, 36664827 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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			031855 bacillus su	_	P45546 escherichia	_	Q00564 lactococcus	•	_	P54219 homo sapien	P58163 caulobacter

ALIGNMENTS

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RIT "NON-Syndromic hearing loss associated with enlarged vestibular radeduct is caused by PDS mutations.";

RI denet 104:188-192(1999).

CC -1- FUNCTION: SODIUM-INDEPENDENT TRANSPORTER OF CHLORIDE AND IODIDE. CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN ADDUT THYROID, LOWER EXPRESSION IN ADULT THYROID, LOWER CC.

CC -1- DISEASE: DEFECTS IN PDS ARE A CAUSE OF PENDRED SYNDROME, AN CC NOT EXPRESSED IN OTHER TISSUES.

CC -1- DISEASE: DEFECTS IN PDS ARE A CAUSE OF PENDRED SYNDROME, AN CC AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONGENITAL SENSORINEURAL HEARING LOSS COMBINED WITH THYROID GOITRE. THE CC DISCASE: DEFECTS IN PDS ARE THE CAUSE OF HEREDITARY CC DEARNESS. THE DEAFNESS IS MOST OFTEN ASSOCIATED WITH A MONDINI CC COCHLEAR DEFECT.

CC AQUEDUCT SYNDROME (EVA); A COMMON FORM OF INNER EAR ABNORMALITY SENSORINEURAL HEARING LOSS COMETIMES PROGRESSIVE SENSORINEURAL HEARING LOSS ARE THE CAUSE OF AUTOSOMAL RECESSIVE SENSORINEURAL HEARING LOSS ARE THE CAUSE OF AUTOSOMAL RECESSIVE SENSORINEURAL HEARING LOSS ARE THE CAUSE OF STRING ASSOCIATED WITH A MONDINI CC SENSORINEURAL HEARING LOSS ARE THE CAUSE OF AUTOSOMAL RECESSIVE SENSORINEURAL HEARING LOSS ARE THE CAUSE OF AUTOSOMAL RECESSIVE DEAFNESS TYPE 4 (DFNB4).
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InterPro; IPR001902; Sulfate_transp.
Pfam; PF001740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
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EMBL; AC002467; AAB88773.1;
MIM; 274600; -.
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Usami S., Abe S.,
Kimberling W.J.;
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MEDLINE-99204606; PubMed-10190331;
Usaml S., Abe S., Weston M.D., Shinkawa H., Van Camp G.,
                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE: NAME-Hereditary hearing loss homepage; NOTE-Gene page; WWW-"http://www.uia.ac.be/dnalab/hhh/hhhgenes.html"
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                                                                                                                                                                                                                                                                                                Transmembrane;
 SULFATE_TRANSP; 1.
Disease mutation; Deafness; Glycoprotein
                       EXTRACELLULAR (POTENTIAL).
8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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SSPAQSEPF	IKSTVGFDA	1	: LTVVLRVQFP	LVVVFQTQFR	KSVLGALIAV :: KSVLAAVVIA	AFGISNIFSG	ALGCSNFFGS	IVKSIPRGFL)IVGEIQRGFF		ITNIASLIFAL	QIGFIVRYLA	QEGEVAIYLS	WACSAATSWE	LVGNICLQLA	SDVISGVSTGI	PLLGGLSGGS	YSELAFQQQH	VYSLTLEDDER	imilarity 3; Conservati	336 3 80 AA;	723 723	721 721	667 667	497 497	416 416	384 384	372 372	369 369	236 236	09	653 673 674 780
ASAEAPGEPSDMLASVPPFVTFHTLILDMSGVS	IRVYNKRLKALRKIQKLIKSGQLRATKNGIIS	APPTDPNNNQTPANGTS		RNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSP	IYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLMRKSKLDCCIWVVSFLSSFFLSLPYGVA	3FFSCFVATTALSRTAVQESTGGKTQVAGIISAAIVMI	DSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLG		PTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLAN		LISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAI	QLIFGGLQIGFIVRYLADPLVGGFTTAAAFQVLVSQLKIVLNVSTKNYNGVLSIIYTLVE	SESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSI	PFPVVSLMVGSVVLSMAPDEHFLVSSSNGTVLNTTMIDTAARDTARVLIASALTLLVGII	PESKFQV-FNNATNESYVDTAAMEAERLHVSATL	VKEWLLSDVISGVSTGLVATLQGMAYALLAAVPVGYGLYSAFFPILTYFIFGTSRHISVG	SIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGV	YMVSRPVYSELAFQQQHERRLQERKTLRESLAKCCSCSRKRAFGVLKTLVPILEWLPKYR	FEKK-DRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLS	30.8%; Score 1190; DB 1; Length 780 35.6%; Pred. No. 5.2e-72; .ive 146; Mismatches 283; Indels	36 L -> M (IN REF. 2). 85722 MW; 3AEF5D720B155CE0 CRC64;		/FTIG=VAR_UU7447. 1								G -> V (I	3 11 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FVDLMG 641	SDAVSTN 612	885 IIASA	::: IFYGNV 559	LYFANS 543	SLPYGVA 483 : LDLGLL 499	43	42	KYDYTI 379	KHGYDV 363	SYGANL 319	SGCKM 303	IYTLVE 259	VETFID 243	LLVGII 199	CLTAII 183	RHISVG 139	/HQMVPG 126	WLPKYR 79	WLPKYK 66); 34; Gaps												

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RESULT 2
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P40879;
01-FEB-1995
01-FEB-1995
20-AUG-2001
                                                                                                               This
                                                                                                                                                                                                                         diarrhea/down-regulated in adenoma gene.";
Hum. Mutat. 11:321-327(1998).
-i- FUNCTION: POSSIBLE SULFATE TRANSPORTER.
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MEDLINE-97051927; PubMed-8890562;
HOEglund P., Halla S., Socha J., Tom
Karjalainen-Lindsberg M.-L., Airola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon adenomas and adenocarcinomas. Proc. Natl. Acad. Sci. U.S.A. 90:41
EMBL; L02785; AAA58443.1; MIM; 126650; -. MIM; 214700; -.
                                            or send an
                                                                                         the
                                                                                                                                                                                                                                                                                              VARIANTS CLD SER-120; ARG-131; VAL-317 DEL MEDLINE-98213471; PubMed-9554749;
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Trends Biochem. Sci.
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MEDLINE=93248250;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                        entities
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Popinska K., Holmbe
                                                                                                                                                                                                                                                                                                                                            congenital chloride diarrhoea.";
                                                                                                                                                                                                                                                                                                                                                    de la Chapelle A., Kere J.;
"Mutations of the Down-regulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a colon mucosa gene that is
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                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
DEVELOPMENTAL STAGE: EXPRESSION IS SIGNIFICANTLY DECREASED IN
ADENOMAS (POLYPS) AND ADENOCARCINOMAS OF THE COLON.
DISEASE: DEFECTS IN DRA ARE THE CAUSE OF CONGENITAL CHLORIDE
DIARRHEA (CLD), A DISEASE CHARACTERIZED BY VOLUMINOUS WATERY
STOOLS CONTAINING AN EXCESS OF CHLORIDE. THE CHILDREN WITH TH
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                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercipean Bioinformatics Institute. There are no restr
                                                                                                                                     SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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                                           non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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. 31, Last sequence 40, Last annotations.
                                                                                                                                                                                                                                                                                                                                                                                                                                  putative human tumour suppressor.";
ci. 19:19-19(1994).
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LTAIIOMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV 238
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                                   VLAIGELLAPLOKSVLAALALGNLKGMLMQFAEIGRLWRKDKYDCLIWIMTFIFTIVLGL
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                                                                     MLVLGIYLYPLPKSVLGALIAVNLKNSLKOLTDPYYLWRKSKLDCCIWVVSFLSSFFLSL
                                                                                                  YDYPLDGNQELIALGLGNIVCGVFRGFAGSTALSRSAVQESTGGKTQIAGLIGAIIVLIV
                                                                                                                              HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT 418
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                                                                                                                                                                                                                InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF007140; STAS; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
PROSITE; PS01130; SULFATE_TRANSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
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J. Biol. Chem. 273:12307-12315(1998).
-i- FUNCTION: SULFATE TRANSPORTER. MA
BONE FORMATION
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MEDLINE-98241598; PubMed-9575183;
Satoh H., Susaki M., Shukunami C.,
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15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG)
SICCEGA2 OR DTDST.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                    Transport;
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DTD_HUMAN
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01-OCT-1996
20-AUG-2001
EMBL; U14528; AAA70081.1; MIM; 222600; -. MIM; 600972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dysplasia sulfate-transporter gene (DTDST): series involving three chondrodysplasias."; Am. J. Hum. Genet. 58:255-262(196).
-i- FUNCTION: SULFATE TRANSPORTER. MAY PLAY
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Cell 78:1073-1087(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Atelosteogenesis type II is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS AO-II GLU-255; TRP-279 A
MEDLINE-96152121; PubMed-8571951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haestbacka J., de la Chapelle A., Mahtani M.M., Clines G., Reeve-Daly M.P., Daly M., Hamilton B.A., Kusumi K., Trivedi B., Weaver A., Coloma A., Lovett M., Buckler A., Kaitila I., Lander E.S. "The diastrophic dysplasia gene encodes a novel sulfate transporter:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=95007757; PubMed=7923357;
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                                                                                  modified and this statement is not removed. entities requires a license agreement (See
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED FOR DIASTROPHIC DISEASE: DEFECTS IN DTDST ARE THE CAUSE OF DIASTROPHIC DISEASE CHARACTERIZED BY (DTD), AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY
                                                                                                                                                                                                                                       DISEASE: DEFECTS IN DTDST ARE THE CAUSE OF ATELOSTEOGENESIS TYPE II (AO-II), ALSO KNOWN AS NEONATAL OSSEDUS DYSPLASIA I, WHICH IS CHARACTERIZED BY SEVERELY SHORPENED LIMBS, SMALL CHEST, SCOLIOSIS CLUB EOOT OF THE EQUINOVARUS TYPE (TALIPES EQUINOVARUS), ABDUCTEI THUMBS AND GREAT TOES, AND CRAFTEN BETTHERE DIE OF RESPIRATORY INSUFFICIENCY SHORPLY AFTER BIRTH BECAUSE OF THE COLLARSE OF THE AIRWAYS AND PULMONARY HYPOPLASIA DUE TO THE SMALL
                                                                                                                                                                                                                                                                                                                                                                            OSTEOCHONDRODYSPLASIA WITH CLINICAL FEATURES INCLUDING DWARFISM, SPINAL DEFORMATION, AND SPECIFIC JOINT ABNORMALITIES.
DISEASE: DEFECTS IN DTDST ARE THE CAUSE OF ACHONDROBNESIS TYPE (ACG-IB). ACG-IB IS A RECESSIVELY INHERITED CHONDRODYSPLASIA CHARACTERIZED BY EXTREMELY POOR SKELETAL DEVELOPMENT AND PERINATERS.
                                                                                                                                        European
                                                                                                                                                                                                          SIMILARITY:
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                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the BMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                    an
                                                                equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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(Rel. 34, Last seq
(Rel. 40, Last ann
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DST): evidence
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Pfam; PF00916; Sulfate_transp;
                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001902;
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                 LTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIP
                                            EAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFG
                                                                                                                                            RPYHRILIERQ
LNLPRTNGVGSLITTWIHVFRNIHKTNLCDLITSLLCLLVLLPTKELNEHFKSKLKAPIP
                                                                      RHISVGIFGVLCLMIGETVDRELQKAGYDNAHSAPSLGMVSNGSTLLNHTSDRICDKSCY
                                                                                       HQMVPGTFAVISILVGNIC---LQ------LAPESKFQVFNNATNESYVDTAAM 165
                                                                                                         WLPKYDLKKNILGDVMSGLIVGILLVPQSIAYSLLAGQEPVYGLYTSFFASIIYFLLGTS 157
                                                                                                                                                                                 226;
                                  -AIMVGSTVTFIAGVYQVAMGFFQVGFVSVYLSDALLSGFVTGASFTILTSQAKYLLG
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31.2%;
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Pred. No. 1.7e
38; Mismatches
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
G -> E (IN AO-II).
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BD613DCB6350D549
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/FTId=VAR_007436.
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G -> V (IN ACG-IB).
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DTD_MOUSE
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AC 06227
DT 01.NO
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DE SULFA
GN SLUFA
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SEQUENCE FROM N.A.
MEDLINE-98036067; PubMed-9370300;
MEDLINE-98036067; PubMed-9370300;
Kobayashi T., Sugimoto T., Saijoh K., Fukase M., Chihara K.;
Kobayashi T., Sugimoto T., Saijoh K., Fukase M., Chihara K.;
Cloning of mouse diastrophic dysplasia sulfate transporter gene
"Cloning of mouse diastrophic dysplasia sulfate transporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTD_MOUSE
Q62273;
Q1-NOV-1997
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG)
SLC26A2 OR DTDST OR DTD.
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EMBL; D42049; BAA07650.1; -. MGD; MGI:892977; Slc26a2. InterPro; IPR002645; STAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: SULFATE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                    BONE FORMATION.
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pfam; pF009216; Sulfate_transp; 1.
pROSITE; pS01130; SULFATE_TRANSP; 1.
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                               NLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFR
                                                                                                                                   TPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGS
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                                                                                                                                                                                                              ESFIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVETFIDICKNLPHTNIASLIFAL
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                                                                                          FFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAV
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EXTRACELLULAR (POTENTIAL)

POTENTIAL.

CYTOPLASMIC (POTENTIAL)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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Pred. No. 2.5e-56;
7; Mismatches 274;
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system of rat hepatocytes.";
J. Biol. Chem. 269:3017-3021(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SULFATE/CARBONATE SAT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P45380;
01-NOV-1995
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            CARBOHYD
                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94132077; PubMed-8300633;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                                                                                                                              InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp
Pfam; PF01740; STAS; 1.
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                                                                                                                                                                                                                                                                                                                                         NOT SUCCINATE AS A CO-SUBSTRATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
TISSUE SPECIFICITY: LIVER, KIDNEY. LESS
                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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(GLCNAC. . GLCNAC. .
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Best Local
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Q94225;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                          Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                  HYPOTHETICAL F41D9.5.
                                                                                                                                                                                           CAEEL
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                                      NCBI_TaxID=6239;
[1]
                                                                                    Caenorhabditis elegans
            STRAIN-BRISTOL N2;
                         SEQUENCE FROM N.A
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AL 85.0 KDA PROTEIN F
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InterPro; IPR001902; Sulfa
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 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitted (APR-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION: POSSIBLE SULFATE TRANSPORTER. SUBCELLULAR IOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
KRYKYKINHGQELYALGFVGVLSSFFPVFPVTSGFARSVVGAAVGGSTQLTCLFSSLALL
                       NKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVM
                                                                                                                                                                                                                                                                                                                   QKLR--YACSPSKCIHSLLSFLPIITWLPKYDWSHSFFGDLSGGLTMAVFSVPQGIALAS
                                                                                                                                                                                                                                                                                                                                          EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFAL 94
                                                                         ISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLA
                                                                                                      YYRIWDLVENLDNVHIPTVCISLSSFLFLVFGKEYLAPWLNSAFNYPVPFELVLLT----
                                                                                                                      VFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHK-IRFPIPTEMIVVVVATA
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                                                                                                                                                                                                            YVNHTLDELLDKENETALISNTTLMQILGNETSFVEEVTMEMWTEGVTPVKQIHVATTII
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PF00916; Sulfate_transp;
TE; PS01130; SULFATE_TRAN
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SULFATE_TRANSP; 1.
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Pred. No. 7.6e-32;
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Proc. Natl. Acad. Sci. U.S.A. 92:9373-9377(1995).

-i- FUNCTION: HIGH-AFFINITY H+/SULFATE COTRANSPORTER THAT MEDIATES

UPTAKE OF SULFATE BY PLANT ROOTS FROM LOW CONCENTRATIONS OF

SULFATE IN THE SOIL SOLUTION.
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P53392;
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                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. VERANO; TISSUE-Root; MEDLINE=96016171; PubMed=7568135; MIDIT F.W., Ealing P.M., Hawkesford M.J., Clarkson "Plant members of a family of sulfate transporters
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Pfam; PF00916; Sulfate_transp;
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                                                                                                                                                                             InterPro; IPR002645;
                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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CT-1996 (Rel. 34, Last sequence update)
CT-1996 (Rel. 34, Last annotation update)
AFFINITY SULPHATE TRANSPORTER 1.
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MEDLINE=96016171; PubMed=7568135;
Smith F.W., Ealing P.M., Hawkesford M.J., Clarkson
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
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Proc. Natl. Acad. Sci. U.S.A.
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NCBI_TaxID=37660;
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327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: HIGH-AFFINITY H+/SULFATE COTRANSPORTER THAT MEDIATES UPTAKE OF SULFATE BY PLANT ROOTS FROM LOW CONCENTRATIONS OF
                                                                                                                       GFVAIYLSESFIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPH-T
                                                                                                                                                                                                                                                                                                  TLFDDEFEKKDRTY----PVGE-KLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYII 72
                                                                                                                                                              LLLGTL---LSNE----ISNTKSHDYL-----
                                                                                                                                                                               GDFIAGLTIASLCIPQDLAYAKLANLDPWYGLYSSFVAPLVYAFMGTSRDIAIGPVAVVS
                                                                                                                                                                                                                                            PDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVIS 132
VKHIKSGVNPSSANEIFFHGK-YLGAGVRVGVVAGLVALTEAIAIGRTFAAMKDYALDGN
                        VGEIQRGF-PTPVSPVVSQWKDMIGTAFSLAIVSYVINL----AMGRTLANKHGYDVDSN
                                                     NWETILIGLSFLIFLLITKYIAKKNKKLFWVSAISPMISVIVSTFFVYITRADKR-GVSI
                                                                             NIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQI
                                                                                                         GFLIDFLSHAAIVGFMAGAAITIGLQQLKGLLGISNNNFTKKTDIISVMRSVWTHVHHGW
                                                                                                                                                                                                                                                                          TLFQEIKHSFNETFFPDKPFGKFKDQSGFR----
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PF01740; STAS; 1.
PF00916; Sulfate_transp;
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Pred. No. 4.1e-27;
8; Mismatches 278
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                                                                                                                                                              RLAFTATF - - FAGVTQMLLGVCRL
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STRAIN=CV. VERANO; TISSUE-ROOT;
MEDLINE-96016171; PubMed-7568135;
Smith F.W., Ealing P.M., Hawkesford M.J.,
""" and members of a family of sulfate trans
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                             Pfam;
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InterPro; IPR001902; Sulfi
                                                                                                                                                                                                                                          EMBL; X82454; CAA57831.1; -.
                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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FUNCTION: LOW-AFFINITY H+/SULFATE COTRANSPORTER WHICH
INVOLVED IN THE INTERNAL TRANSPORT OF CONTRACTE BETWEEN
SUBCELLULAR COMPARTMENTS WITHIN THE PLANT.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTEN
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE FAMILY.
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          HGGVFEDGSLECKHVFPSIHDAV
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Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetes;
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; 031900; AAA97582.1; -
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InterPro; IPR002645; STAS.
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SULX_YEAST STANDARD; PRT; 7
P53394;
P53394;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last anotation
PUTATIVE SULFATE TRANSPORTER YPRO03C.
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
Badcock K., Bowman S., Churcher C.M., Pearson
Walsh S.V., Barrell B.G.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
-!- FUNCTION: POSSIBLE SULFATE TRANSPORTER.
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                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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PS01130; SULFATE_TRANSP; FALSE_NEG
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                                                                                      IFDLGGMTSIDSSAAQVLEEIITSYKRRNVFIYLVNVS--
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Pred. No. 9e-22;
8; Mismatches 265;
VAASVERAQANNNENNTSNTFSDA-GETYSPYFDS
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EMBL; U53880; AAB67596.1;
EMBL; 273264; CAA97653.1;
EMBL; 273265; CAA97655.1;
EMBL; U53876; AAB67550.1;
SGD; S0004082; SUL2.
                                                                                                                                                                         InterPro; IPR002645;
InterPro; IPR001902;
Pfam; PF01740; STAS;
Pfam; PF00916; Sulfat
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., K
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.
Johnston L., Langston Y., Latreille P., Le T., Mardis E.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P.
Wilson R., Waterston R.;
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                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                  in Saccharomyces cerevisiae.";
Genetics 145:627-635(1997).
-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; /
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
SULFATE PERMEASE 2 (HIGH-AFFINITY SULFATE TRA
SUL2 OR SEL2 OR YLR092W OR L9449.1
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Q12325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Surdin-Kerjan Y.; 
"Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97207837; PubMed=9(
Cherest H., Davidian J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Benes V., Rechmann S
Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                          or send
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                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                PS01130;
                                                                  Transmembrane;
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164
1184
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o the EMBL
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                   Glycoprotein
POTENTIAL
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                                                                                                                                                                 TRANSP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas
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EMBL/GenBank/DDBJ da
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POTENTIAL.
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STRAIN=INVSC1;
MEDLINE=95342164; PubMed=7616962;
MEDLINE=95342164; PubMed=7616962;
Smith F.W., Hawkesford M.J., Prosser I.M., Clarkson D.
Smith F.W., Hawkesford M.J., Prosser I.M., Clarkson D.
"Isolation of a cDNA from Saccharomyces cerevisiae tha
"Isolation of a cDNA from Saccharomyces cerevisiae tha
high affinity sulphate transporter at the plasma membr
Mol. Gen. Genet. 247:709-715(1995).
                                                                                                                                                                                                                                                                            SUL1_YEAST
P38359;
01-OCT-1994
                                                                                                                                                                                                                                                                                                                               _YEAST
                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SULFATE PERWEASE 1 (HIGH-AFFINITY SULFATE TRANSPORTER
SUL1 OR SFP OR YBR294W OR YBR2110.
                                                                                                                                                             Eukaryota; Fungi; P
Saccharomycetales;
                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SDMLASVPPFVTFHT 626
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                                                                                                                                                                Saccharomycetaceae;
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8; Mismatches
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                                membrane.";
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Вþ Š 망

108

PIIKWFPHYNF-TWGYADLVAGITVGCVLVPQSMSYAQIASLSPEYGLYSSFIGAFIYSL

PVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFF

VNSSKQKFGYTKNELSDYLYDSIPAYEESTYTLKEYYDHSIKNNLTAKSA--GSYLVSLF MSQPRPRYVVDRAAYSLTLFDDEFEKKDRTYPVGE----KLRNAFRCSSAKIKAVVFGLL

107 56

57 50 Matches

Similarity

156;

.1e-17

Indels

184;

Gaps

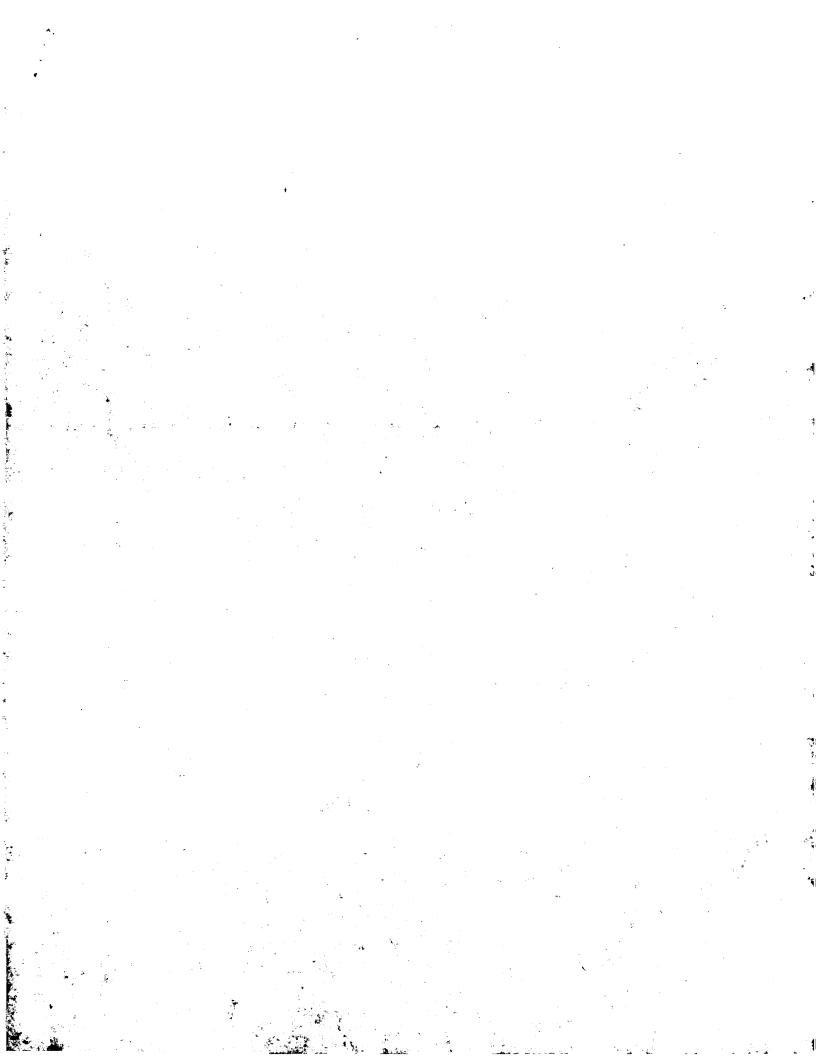
31;

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Query Match
Best Local s
                                                 TRANSMEM
CONFLICT
CONFLICT
SEQUENCE
                                                                                        TRANSMEM TRANSMEM
                                                                                                            TRANSMEM TRANSMEM
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                                                                                                                                                                                                                                                            SGD;
                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    in Saccharomyces cerevisiae.";
Genetics 145:627-635(1997).
-!- FUNCTION: HIGH AFFINITY UPTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jin Y.H., Jang Y.K., Kim M.J., Park S.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fritz C., Hollenberg
Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C;
Fritz C., Hol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM
                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surdin-Kerjan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cherest H., Davidian J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                  Transport;
                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                EMBL; Z36163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY. CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE FRAMESHIFT IN POSITION 488.
                                                                                                                                                                                                                                                                   ; x82013; CAA57540.1;
; z35134; CAA84506.1;
S46176; S46176.
                                                                                                                                                                                                                                                           S0000498;
                                                                                                                                                                                                           PS01130;
                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long
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IPR001902; Sulfa
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95950 [
           9.7%;
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                                                                                                                                                                                                                     _transp;
                                                                                                                                                                                                  Glycoprotein
                                                                                                                                                                                                                                                                              ALT_FRAME
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Score 377; DB
Pred. No. 1.1e
56; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Similarities between a soybean nodulin, Neurospora crassa sulphate permease II and a putative human tumour suppressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandal N.N., Marcker K.A.;
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InterPro; IPR001902;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen
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A; Residues: 1-764 < RES>
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probable sulfate t	2 C64867	0	55	6.0	230.5	45
hypothetical prote	2 D85700	0	55	6.0	230.5	44
sulfate permease f	2 D82303	2	54	6.2	238	43
integral membrane	2 576624		55	6.4	249.5	42
sulfate permease I	2 A37956	1 2	781	6.5	250	41
sulfate permease f	2 A82505		55	7.4	286.5	40
probable sulfate t			66.	8.1	313	39
probable sulfate t	2 C83642	7 2	51.	8.2	315.5	38
hypothetical prote	F70688		56	9.4	365.5	37
sulfate permease f			59:	9.6	372	36
sulfate transport	2 S34800		48	9.7	375.5	35
sulfate transport			85	9.7	376	34
high affinity sulf	2 S74633	2	561	10.0	386	ω u
probable membrane	2 \$64926		89	10.5	405	32
probable membrane	2 S52816	2	75,	11.3	437	31
protein F28K19.22	D96809	2	719	11.4	441.5	30

ALIGNMENTS

A;Cross-references: GB:L02785; NID:g291963; PID:g291964 C;Genetics: A;Gene: GDB:DRA A;Cross-references: GDB:138165; OMIM:126650 A;Map position: 7q22-7q31.1 C;Superfamily: sulfate transport protein C;Keywords: tumor suppressor C;Accession: A47456
R;Schweinfest, C.W.; Henderson, K.W.; Suster, S.; Kondoh, N.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 4166-4170, 1993
A;Title: Identification of a colon mucosa gene that is down-regulated in colon adenom A;Reference number: A47456; MUID:93248250
A;Accession: A47456 down-regulated in adenoma (DRA) - human
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 26-Aug-1999 A;Status: preliminary; translated from GB/EMBL/DDBJ 359 7 RYVVDRAAYSLTLFDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65 LTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV 238 GGCXMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK KVLYSVESQIEKTNIADLVTALIVLLVVSIVKEINQRFKDKLPVPIPIEFIMTVIAAGVS GPFPILSMMVGLAVSGAVSKAVPDRNATTLGLPNNSNNSSLLDD---ERVRVAAAASVTV 184 GTFAVISILVG----NICLQLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLAC 178 RLKEWLLSDIVSGISTGIVAVLQGLAFALLVDIPPVYGLYASFFPAIIYLFFGTSRHISV 127 KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125 QYIVARPVYSTNAFEENHKKTGRHHKTFLDHLKVCCSCSPQKAKRIVLSLFPIASWLPAY 67 HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT 418 YGCDFKNRFKVAVVGDMNPGFQPPITPDVETFQNTVGDCFGIAMVAFAVAFSVASVYSLK LSGIIQLAFGILRIGFVVIYLSESLISGFTTAAAVHVLVSQLKFIFQLTVPSHTDPVSIF Conservative 28.9%; Score 1120; 34.0%; Pred. No. 2 142; Mismatches DB 2; 2.9e-78; Length 764; Indels 68; Gaps 364 298 304 244 11;

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A54808

A54808

diastrophic dysplasia-associated sulfate transport protein - human
C;Species: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Accession: A54808
R;Haestbacka, J; de la Chapelle, A.; Mahtani, M.M.; Clines, G.; Reeve-Daly, M.;
der, E.S.
Cell 78, 1073-1087, 1994
A;Title: The diastrophic dysplasia gene encodes a novel sulfate transporter: pos
A;Reference number: A54808; MUID:95007757
A;Accession: A54808
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-739 <HAE>
A;Cross-references: GB:U14528
C;Genetics:
A;Gene: GDB:DTD; DTDST
A;Map posttion: 5q3-5q33.1
C;Superfamily: sulfate transport protein
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LTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIP
                                                                                                                                                                                  WLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGV 120
                                                                                                                                                                                                                             RPYHRILIERQ----
                                             ---AIMVGSTVTFIAGVYQVAMGFFQVGFVSVYLSDALLSGFVTGASFTILTSQAKYLLG
                                                             HQMVPGTFAVISILVGNIC---LQ------LAPESKFQVFNNATNESYVDTAAM 165
                                                                                                                                                                  WLPKYDLKKNILGDVMSGLIVGILLVPQSIAYSLLAGQEPVYGLYTSFFASIIYFLLGTS
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Pred. No. 1.5e-66;
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A,Cross-references: GB:L23413; NID:g431452; PIDN:AAA17545.1; PID:g431453 C;Superfamily: sulfate transport protein C;Keywords: glycoprotein; transmembrane protein
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A49994
A49994
Sulfate transporter, canalicular - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jan-1995 #sequence_revision 20-Jan-1995 #text_change 24-Sep-1999
C:Accession: A49994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: AcA; Accession: A49994
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bissig, M.; Hagenbuch, B.; Stieger, B.; Koller, T.; Meier, P.J. J. Biol. Chem. 269, 3017-3021, 1994
A;Title: Functional expression cloning of the canalicular sulfate A;Reference number: A49994; MUID:94132077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-703 <BIS>
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                                                                                                                                                                                                                                   36 KLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALL 95
                                                                                                                                      ANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNIC---LQLA-----
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                                         -PESKFQVFNN-ATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSE
                                                                                          AGLQPIYSLYTSFFANLIYFLMGTSRHVNVGIFSLLCLMVGQVVDRELQLAGFDPSQDSL
                                                                                                                                                                                       RLKKSCTCSMPCAQALVQGLFPVIRWLPQYRLKEYLAGDVMSGLVIGIILVPQAIAYSLL
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                                                                                                                                                                                                                                                                                 201;
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29.3%;
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Pred. No. le-57;
3; Mismatches 3
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A; Dolecule type: DNA
A; Molecule type: L-611 <WIL>
A; Residues: 1-611 <WIL>
A; Cross-references: EMBL: Z70757; PIDN: CAA94798.1; GSPDB: GN00023; CESP: ZK287.
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone C; Genetics: A; Gene: CESP: ZK287.2
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R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZK287.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A;Introns: 3/3; 102/1; 438/3
C;Superfamily: sulfate transport protein
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YLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLI 257
                                       ARLRLAPD -- IPISNSSDINPSVYPLGEYVDPLVFTSALTLLVGVVQIIMGILRLGFLTT
                                                                                                                    GLTVGIMHVPQGMAYASLAGVPPVYGMYSSFFASTIYMFFGTARHISIGVFAVASMMVGA 113
                                                                                                                                                                                                 TTTDQDIVEKKECSPFRKKLQK------YIPILEWLPNYQWKDHFHGDVIA 53
                                                                                                                                                                                                                                      TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLG 77
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                                                                          ICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAI 197
                                                                                                                                                         GLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGN 137
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                                                                                                                                                                                                                                                                                  al Similarity
197; Conser
                                                                                                                                                                                                                                                                                20.2%; Score 781; DB 2 clarity 28.3%; Pred. No. 3e-52; Conservative 138; Mismatches 2
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A;Introns: 48/3; 128/1; 165/1; 220/3; 407/3; 471/3; 503/3; 539/2; C;Superfamily: sulfate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: Z19774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K12G11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jan-2000 C;Accession: T23628
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-749 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T23628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: R; Kershaw, J.
                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: K12G11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIASALSSFFPVYPVGASLSRSSVCEMSGANTQLYTIFSSFLLLTVILLLGPFLEPLPMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEIPRGFPLPSIPRLNFLPALLSDAIPIAVVCYMFVMSMGKLFAKKHKYKTDATQELYAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIAL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALISGAFLVLVKELNARYMHKI-----RFPIPTEMIVVVVATAISGGCKMPKKYHMQIV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPRPRYV--VDRAAYSLTLEDDEFEKKDRTYPVGEKLRNAFRCSSAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEP 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVLRQQWP---SFSTVLHDE---TPR----QNVPENVKIVKFAGSLHFANVTAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILACIVIVSLKSLFMQVKELPRLYRISKYDFAIWLVACLSTIFTDVTTGLVISLAFSLYT
TSLFPPLIYMLFGTSRHASLGTFAVVSLMTGLSVEKLAAPTDYD--PSSFNETDIDLVKL
                             SSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAM 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDV 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDI-QGIKIITYCSPLYFANSEIFRQKVI
                                                                                                                                  SEPNKRRVSFVQRGAMNQAQFDEKF----DYNKP----HLENELKKQAKKFVRRFYEPFTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISI----FGILFLDLGRTYINPIVKKFSPIPPPLELILVIFGIVISMIFNLDAEYHVKTV
                                                                                                                                                                                                   206;
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                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                   20.1%;
28.2%;
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                                                                                                                                                                                                  ; Score 776.5; 1
; Pred. No. 8.9e
142; Mismatches
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                                                                                                                                                                                                                   8.9e-52;
                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                   311;
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                   71;
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submitted to the EMBL Data Library, November
A:Reference number: Z19774
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A; Introns: 26/3; 55/2;
C; Superfamily: sulfate
                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-700 <WILD:
A; Cross references: EMBL: 281570;
A; Experimental source: clone K12G
                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T23629
                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K12G11.2 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T23629
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Best Local
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                                                             RAAYSLTLFDDEFEKKDRTYPVGEKLRNAFRCSS------AKIKAVVFGLLPVLSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFP 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMRDATSIAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAPMNQVEYDEKYGYQKRLKDGGKFKKRSTKVASRYYVPFTSVTNFKIFLLNLFPIFGWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSGFTFIDLMGVSALKEIFSDMRKRGILVYFANAKAPVREMFEKCHFFNFVSKE--NFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTPANG----TSVSYI-TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPIPWELVIVILSTVFVAVTGVDTEAKVQVVNKIPVGVPNFSLPSFYLIPQVLPDAISIT
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                                                                                                         Similarity
                                                                                              Conservative
                                                                                                                                                                       107/1; 197/3; 253/3; transport protein
                                                                                                           19.9%;
                                                                                         98; Score 768; DB 2; Lo
98; Pred. No. 3.7e-51;
141; Mismatches 322;
                                                                                                                                                                                                                                                                   PIDN:CAB04607.1; GSPDB:GN00023;
                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                                                                     307/3;
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                                                                                                                                                                                       335/2;
                                                                                                                         Length
                                                                                            Indels
                                                                                                                                                                                       480/3;
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                                                                                            40;
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                                                                                                                                                                                       516/2;
                                                                                                                                                                                                                                                                   CESP: K12G11.2
                                                                                         Gaps
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VYFASTKVPVREMFEKCSFFDFVSKE--NFYPTLRDATGIAR
                   VFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQ 700
                                                                                                                            LFHNVECFK-KCIEKVYDEWKKSSEF------NFVKEPNAGKGSKFTFEGMHRIAPI
                                                                                                                                                        YFANSEIFROKVIAKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQ
                                                                                                                                                                                                           PYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPL
|: : |:: : |: : : | : : | | | | | | | : : : | : : | | : : | | |
                                                                                                                                                                                                                                                                         MLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSL 478
                                                                                                                                                                                                                                                                                                                     YEYEIDAGQELYALSFTAIGGSFFPTFPTSIGLGRTMVGVESGVKTQVATFFSCLFVLSV
                                                                                                                                                                                                                                                                                                                                              HGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDICKNLPHTNIASLIFALISGAFLVLVKE-LNARYMHKIR--FPIPTEMIVVVVATAIS
                                                                                            SEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGVK
                                                                                                                                                                                         SEGLLIAIFFALFTTILREQYPKWHLLANVKDTDEFSDTQQYQETIFYKGICIFKFDAPL
                                                                                                                                                                                                                                                      SLYFGRFLETLPMCVLSAIIVIALKSMLWKLRDLKGIWKLSKIDCCIWMVAFFATVLVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLT-IPSYTGPGSIVFTF
                                                             ---PILPRH-FVIDCSGFTFIDLMGVSALKEVFSDLRKKRVQ
   695
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RESULT 7
T16077
T16077
hypothetical protein F14D12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16077
R;Minx, P.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F14D12.
A;Reference number: Z18457
A;Reference number: Z18457
A;Accession: T16077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-650 <MIN>
A;Residues: 1-650 <MIN>
C;Genetics:

Вþ Š Matches 179; Query Match Best Local : 25 4 EKKDRTYP-----VGEKLRNAFRC---SSAKIKAVVFGLLPVLSWLPKYKIKDYII 72 EEYDQMYSFNREGNETWVKKKINN--YCTFLSKDGIRKIILRRVPVIDWIGSYQINNF-A 60 Similarity Conservative 16.3%; 24.1%; 145; Score 631; DB 2; Pred. No. 1.2e-40; 5; Mismatches 290 Length 650; Indels 128; Gaps 17;

A;Gene: CESP:F14D12.5
A;Introns: 3/3; 53/2; 77/1; 159/3; 181/2; C;Superfamily: sulfate transport protein

215/3;

270/3;

321/1;

443/3;

479/2;

503/3;

CESP:F1

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A;Cross-references: EMBL:U67954; PIDN:AAB52608.1; GSPDB:GN00028; CESP:F41D9.
A;Experimental source: strain Bristol N2; clone F41D9
C;Genetics:
                                                                                                                                                                                                                                    RESULT 8
T25751
T25751
C; Apecies: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C; Accession: T25751
R; Fulton, B.
   A; Map position:
A; Introns: 5/3;
C; Superfamily: s
                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-758 <FUL>
                                                                                                                                                                                      A; Description: The sequence of A; Reference number: Z20081
                                                                                                                                                                                                      submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmi
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                                                    CESP: F41D9.5
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74/1; 111/1; 165/2; 206/:
sulfate transport protein
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                   261/3;
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                 313/3;
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                   370/3;
                   466/3;
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hypothetical protein W04G3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T26165
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T26165
                   R; Lennard,
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                   Z.
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1; Mismatches 295;
November
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submitted to the EMBL Data Library, Nov A;Reference number: Z20163 A;Accession: TZ6165 A;Status; preliminary; translated from GB/EMBL/DDBJ

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A; Experimental source: C; Genetics: A; Molecule type: DNA A; Residues: 1-380 <WIL> A; Cross-references: EMB EMBL: Z68014; PIDN: CAA92028.1; clone W04G3 GSPDB:GN00028;

CESP: W04G3

A;Gene: CESP:w04G3.6 A;Map position: X A;Introns: 46/1; 83/1; 135/3; 153/3; 190/3; 244/3; 272/2

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Lil, J.H.; Lil, Y.; Liln, X.; Lilu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; Reference and analysis of chromosome 1 of the plant Arabidopsis.
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C; Superfamily: sulfate transport protein
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A;Molecule type: DNA
A;Residues: 1-631 <STO>
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    198
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                                                                                                                                                                                                                                                              TLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLLG 77
                                                                                                                                                                                                                    TFFPDDPLRQFRGQPNRTKL------IRAAQY-IFPILQWCPEYSF-SLLKSDVVS 72
YLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTN-----
                                                MLRQ-----
                                                                                                                               GLTIASLAIPQGISYAKLANLPPIVGLYSSFVPPLVYAVLGSSRDLAVGPVSIASLILGS 132
                                                                                                                                                             GLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGN 137
                                                                                     ICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAI 197
                                                                                                                                                                                                                                                                                                               nucn 14.2%; Score 549; DB 2; al Similarity 26.0%; pred. No. 2.5e-34; 175; Conservative 120. winner:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVIAKKHNYEIDVRQEFFALGIVASTCSMFPCWPATTALARTLINDNAGTKTQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPITKWLPNYSISENLINDIIGGVTVGILNVPQGMAYASLVGLKPVYGLYTSLFPSLIYM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLAVGLTQIIMGLFKANYLISYLSDQIILGFTTGAAVHVLTAQLNKILGVALPRHSGIG
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33.6%; Pred. No. 4.6e-35;
tive 78; Mismatches 148;
                                           SPVDDPVLFLQ-LAFSSTF--FAGLFQASLGILRLGFIID 175
                                                                                                                                                                                                                                                                                                               120; Mismatches 251; Indels 126;
                                                                                                                                                                                                                                                                                                                                                      Length 631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sulfate transporter ATST1 [imported] - Arabidopsis thaliana (;Speckes: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_ch.C;Accession: T48901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-658 <SOH>
A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Sohlberg, L.E.; Sussex, I.M.
Plant Physiol. 113, 1463, 1997
A;Title: Nucleotide sequence o.
A;Reference number: Z15626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: D89631; A; Experimental source: Landsberg
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A; Status: preliminary; translated
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                                                                                                                                                                                                                                         4 PRPRYVVDRAAYSL--TLF-DDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGL---LP 57
                                                                                                                               VLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFL 117
                  GSSRDLAVGTVAVASLLTG---AMLSKE---
                                                            GGVHOMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----LHV 172
                                                                                                        IFEWAPRYNLK-FFKSDLIAGITIASLAIPQGISYAKLANLPPILGLYSSFVPPLVYAVL 128
                                                                                                                                                                                             PQPQPFLKSLQYSVKETLFPDDPFRQ-----FKNQNASR-----KFVLGLKYFLP
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                                                                                                                                                                                                                                                                                     14.1%; Score 544.5; DB 2; ilarity 24.9%; Pred. No. 5.8e-34; Conservative 127; Mismatches 274;
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A;Molecule type: DNA
A;Residues: 1-658 <ALC>
A;Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.10
A;Experimental source: cultivar Columbia; BAC clone F4F15
C;Genetics:
                                                                                                                                                                                                                                                                                                                      sulfate transporter (ATST1) - Arabidopsis thaliana
N;Alternate names: protein F4F15.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T49069
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
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A; Accession: T49069
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                                                                                                                                                    ;Map position: 3
;Introns: 116/1; 185/2;
;Superfamily: sulfate to
                                                                                              Query Match
Best Local Similarity
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·58 VLSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFL
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                                                                                                                                                                                              ATSP: F4F15.10
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                                             SFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKVDKFDFLVCMSAYVGVVFGSVEIGLVVAVAISIARLLLFVSRPKTAVKGNIPNSMIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYV 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNYNAGCKTAMSNIVMAIAVMFTLLFLTPLFHYTPLVVLSAII-ISAMLGLIDYQAAIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VATA-----SPVVSQWKDMIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFTATFFAGVLEASLGIFRLGFIVDFLSHATIVGFMGGAATVVSLQQLKGIFGL--KHFT
                           PQPQPFLKSLQYSVKETLFPDDPFRQ-----FKNQNASR-----KFVLGLKYFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTPANG-TSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696
                                                                                   Conservative 127;
                                                                                                                                                    transport protein
                                                                                                                                                                   242/3; 264/3; 302/3;
                                                                                              14.0%; Score 543.5; DB 24.9%; Pred. No. 7e-34;
                                                                                   Mismatches
                                                                                                                                                                   341/3; 384/1; 479/3; 543/2; 572/1;
                                                                                   274;
                                                                                                                                                                                                                                                                                                                          R.; Mewes, H.W.; Rudd, S.; 2000
                                                                                                           2;
                                                                                   Indels 141;
                                                                                                             Length
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                           Query Match
Best Local
                                                                                                                           Genetics:
             Matches
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             180;
                           Similarity
              Conservative
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hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000 C;Accession: T51161
                                                                                                                                      A;Map position: 3
A;Introns: 161/1; 230/2
C;Superfamily: sulfate
                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-703 <C
                                                                                                                                                                                                                                                                                                                           A;Accession: T51161
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Fine sequence analysis of 60 kb around the A; Reference number: 224835; MUID: 20108326
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, Plant Mol. Biol. 41, 687-700, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 GNIDTSGISMMVEIKKVIDRRALKLVLSNPKGEVVKKLTRSKFIGD-HLGKEWMFLTVGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTPANG-TSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTEQYPSSRTVPGILILEIDAPIYFANASYLRERIIRW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNYNAGCKTAMSNIVMAIAVMFTLLFLTPLFHYTPLVVLSAII-ISAMLGLIDYQAAIHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----LHV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230/2; 287/3; 309/3; 347/3; lfate transport protein
                                                                                                                                                                                                                                                                             <COM>
                                                                                                                                                                                                                                                   EMBL: AF049236; PIDN: AAC14417.
14.0%; Score 543.5; DB 2; 24.9%; Pred. No. 7.7e-34; tive 127; Mismatches 274;
                                                                                                                                                                   386/3; 429/1; 524/3; 588/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana AtEml locus
                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.; Delseny, M.; Grellet,
                                                            703;
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Indels

141;

Gaps

23;

642/

C; Superfamily:

sulfate

transport

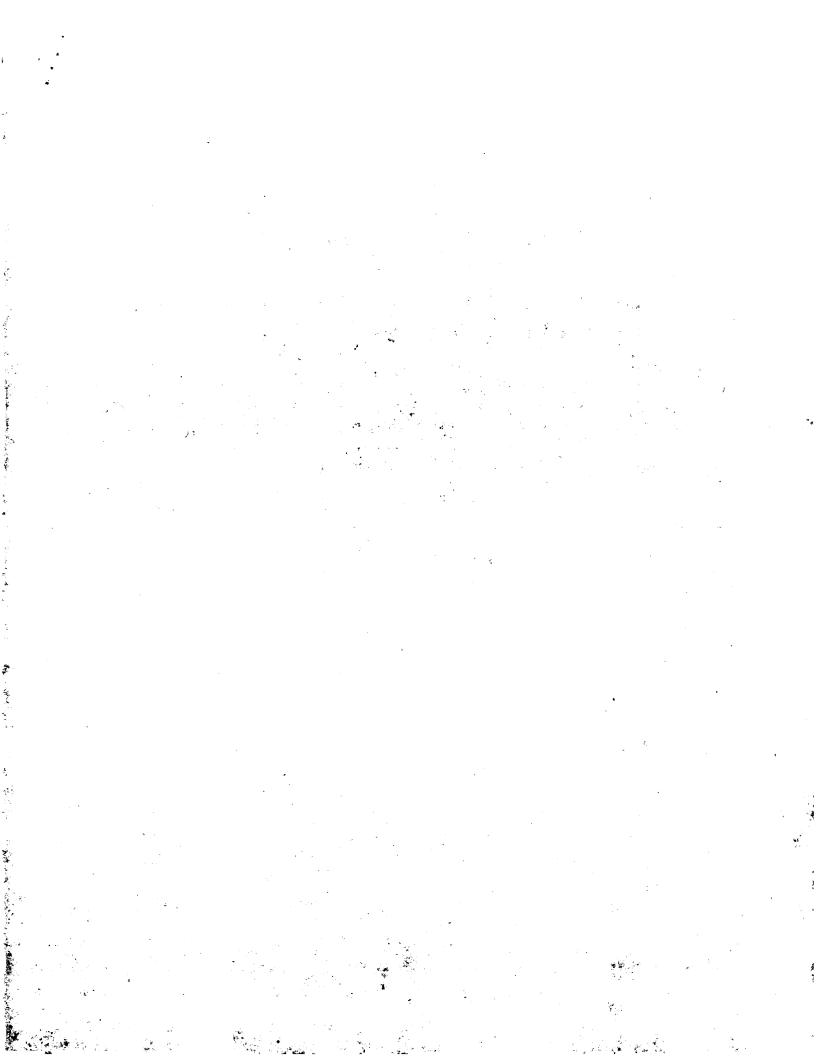
protein

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hypothetical protein W01B11.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te) C;Accession: T32945 R;Bradshaw, H.; Graves, T.; Blair, T. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid W01B11 A;Reference number: Z21250 A;Accession: T32945
A;Gene: CESP:W01B11.2
A;Map position: 1
A;Introns: 15/2; 38/3;
                                                                                       A; Cross-references: EMBL: AF043704; A; Experimental source: strain Bris: C; Genetics:
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        38/3;
        114/1;
        269/3;
                                                                                                                 N704; PIDN:AAB97595.1; GSPDB:GN00019; Bristol N2; clone W01B11
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  420/1; 497/1; 518/2;
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     648/1;
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sulfate transporter AST12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_ch. C;Accession: T48902
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T48902
A;Status: preliminary;
A;Molecule type: DNA
                              A; Title: Identification of two A; Reference number: Z25001 A; Accession: T48902
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                                                                                       R;Takahashi, H.;
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                                                                                                                                                                              15
                                                                                                                                                                                                                       VSVSDAVDQAELEQRHKTETVQTTAAP
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                                                                                                                                                                                                                                                                                               DMSGVSFVDLMGIKALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFPIPTEMIVVVVATAISGGCKMPKKYHMQI--VGEIQRGFPTPVSPVVSQWKDMIGTAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLT-IPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHK---I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQV-FNNATNESYVD-----TAA
                                                                                                                                                                                                                                                                                DCSTIIYVDLMGQGALKDVYNDYKTIGISVLFANTNEHVRQNFETSQFFEE--VPRGRMF
                                                                                                                                                                                                                                                                                                                                                                  TDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLIL
                                                                                                                                                                                                                                                                                                                                                                                                 IKIFRFDSPIYFGNSEMFVRKIHQACGLNPLIVRGELETENKKKDARKEKEEEDAEIPKE
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                                                                                                                                                                                                                                                                                                                                       TEKE----TKLEVTTHQAKVLDEKHAEPEPN---PADQYERLTHI-
                                                                                                                                                                                                                                                                                                                                                                                                                         IKIITYCSPLYFANSEIFRQKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFCVWRSCWMYSALAETGARVDCGCCDEGLVHSDFHLLRVEEIEFCGLCELRGGKPGVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YALFGTSKHSSPGAFAIVSLMVGTVV-----ESFGDVGSTNGTIDSNVDLLCCRENKPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                     Sasakura, N.;
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                  translated
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23.8%;
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                                                                                        Kimura,
                                                            leaf-specific sulfate
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Pred. No. 6.6e-33;
                  from
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                  GB/EMBL/DDBJ
                                                                                        Watanabe,
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                                                                                        Α.,
                                                            transporters
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                                                                                       Saito,
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A;Residues: 1-646 <TAK>
A;Cross-references: EMBL:AB012048; PIDN:BAA25175.1
A;Cross-references: EMBL:AB012048; PIDN:BAA25175.1
A;Experimental source: ecotype Columbia
C;Genetics:
C;Genetics:
A;Map position: 3
A;Introns: 116/1; 185/2; 242/3; 264/3; 302/3; 329/3; 372/1; 467/3; 531/2; 560/1; 585/3
C;Superfamily: sulfate transport protein
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                                                                                                                                                                                                                                                                                                                                                                                   332
                                                                                                                                                                                                                             451
                                                                                                                                                                                                                                                                                                    392 IVMAIAVMETLLELTPLEHYTPLVVLSAII-ISAMLGLIDYQAAIHLWKVDKFDELVCMS
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                                                                                                                                                                                                                                                                                                                                                                                                    349 LAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVAS 408 :|:||: | | | |: :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AFTATFFAGVLEASLGIFRLGFIVDFLSHATIVGFMGGAATVVSLQQLKGIFGL--KHFT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
575 IKKVIDRRALKLVLSNPKGEVVKKLTRSKFIGD-HLGKEWMFLTVGEAV 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 VATAISGGCKMPKKYHMQIVGEIQRG----FPTPVSPVVSQWKDMIGTAFSLAIVSYVIN 348
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                                                                                                                                                                                                                                                                                                                                                                     GPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVV 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----LHV 172
                                 LSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAV 696
                                                                                                            TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAK 647
                                                                                                                                                                                     IKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNNQTPANG-TSVSYI 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSRDLAVGTVAVASLLTG---AMLSKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQPQPFLKSLQYSVKETLFPDDPFRQ-----FKNQNASR-----KFVLGLKYFLP 69
                                                                         ------ILDMSAVGNIDTSGISMMVE
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                                                                                                                                                                                                                                                                                                      450
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Search completed: April 26, 2002, 09:06:02 Job time: 208 sec



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Minimum
Maximum
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-1819-677-049-9
US-08-1319-675-2
US-09-110-116-3
US-08-861-464-4
US-08-138-6011-464-4
US-08-138-9916-2
US-08-988-976-2
US-08-988-968-7
US-08-988-968-7
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7 RYVVDRAAYSLTLFDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65

Matches

250;

Conservative

142;

Mismatches 275;

Indels

68;

Gaps

11;

Query Match 28.9%; Score 1120; DB 1; Length Best Local Similarity 34.0%; Pred. No. 1.7e-101;	RESULT 1 US-08-424-567-2 Sequence 2, Application US/08424567 Patent No. 5569755 GENERAL INFORMATION: Colon Mucosa Gene Having Down-Regul TITLE OF INVENTION: Expression In Colon Adenomas And A APPLICANT: PAPAS, Takis S. APPLICANT: PAPAS, Takis S. APPLICANT: PAPAS, Takis S. CORRESPONDENCE ADDRESS: ADDRESSE: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C. COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATEININ Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/424,567 FILING DATE: 05-MAR-1993 ATTORNEY/ACENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 20,20672-5309 TELEEY: 904136 INFORMATION FOR SEQ ID NO: 2: SOUGHLE TYPE: protein US-08-424-567-2	ALIGNMENTS	28 99 2.6 574 3 US-09-042-913-7 29 99 2.6 574 3 US-09-188-496-6 30 99 2.6 574 3 US-09-042-937-7 31 99 2.6 574 4 US-09-397-238A-4 32 96.5 2.5 401 3 US-08-492-459-6 33 96.5 2.5 401 3 US-08-492-459-28 36 96.5 2.5 401 3 US-08-492-459-28 37 96.5 2.5 401 3 US-08-423-752-8 38 96.5 2.5 401 3 US-08-423-752-8 39 96.5 2.5 401 4 US-08-716-873-20 40 96.5 2.5 401 4 US-08-716-873-22 41 96.5 2.5 401 4 US-08-716-873-22 42 96.5 2.5 401 4 US-08-716-873-42 43 96.5 2.5 401 4 US-08-716-873-42 44 96.5 2.5 401 4 US-08-716-873-43 45 96.5 2.5 401 4 US-08-716-873-42 46 96.5 2.5 401 4 US-09-368-431-20 47 96.5 2.5 401 4 US-09-368-431-20
Leng	wn-Re s And		Sequence 7, Appli Sequence 6, Appli Sequence 4, Appli Sequence 8, Appli Sequence 8, Appli Sequence 28, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 20, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 23, Appli Sequence 42, Appli Sequence 43, Appli Sequence 43, Appli Sequence 6, Appli Sequence 6, Appli Sequence 22, Appli

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US-08-711-928-2

: Sequence 2, Application US/08711928

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APPLICANT: SCHWEINFEST, Clifford W.
APPLICANT: PAPAS, Takis S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                      TITLE OF INVENTION: Colon Mucosa Gene Having Down-Regulated TITLE OF INVENTION: Expression In Colon Adenomas And Adenoc NUMBER OF SEQUENCES: 8
                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W CITY: Washington, D.C.
                                                                                    COUNTRY:
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Best Local :
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/354/NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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LENGTH: 764 amino acids
TYPE: amino acid
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APPLICATION NUMBER: U
FILING DATE: 05-MAR-
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YFANSEIFRQKVI------AKTVSLQELQQ-----
                                                GLGLAASVAFQLLTIVFRTQFPKCSTLANIGRTNIYKNKKDYYDMYEPEGVKIFRCPSPI
                                                                          PYGVAVGVAFSVĹVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPL 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTFAVISILVG----NICLQLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLAC 178
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                                                                                                                                                                                                                                                                                                                                                                         GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK 358
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Best Local :
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                                                                                                                                                                                                                                 TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 40 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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CLASSIFICATION:
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             KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125
                                      QYIVARPVYSTNAFEENHKKTGRHHKTFLDHLKVCCSCSPQKAKRIVLSLFPIASWLPAY
                                                              RYVVDRAAYSLTLFDDEFEKKDRTYPVG-EKLRNAFRCSSAKIKAVVFGLLPVLSWLPKY 65
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Pred. No. 1.7e-101;
2; Mismatches 275;
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US-08-471-496-2
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APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN
NUMBER OF SEQUENCES: 9
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CURRENT APPLICATION NUMBER: US/08/471,406
FILING DATE: 06-JUN-100
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                   STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                       STATE:
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VKSSIFFLTIHDAVL 718
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1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                   USA
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ORK AVENUE, SUITE 600
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; MOLECULE TYPE:
US-08-471-496-2
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                                                                                                                                                                                                                                                      Sequence 2, Application US/08894840 Patent No. 5859200
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Best Local :
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-250 INFORMATION FOR SEQ ID NO:
                                                                                                                      APPLICANT: CAO, LIANG A. APPLICANT: ROSEN, CRAIG A. TITLE OF INVENTION: HUMAN AMINE TRANSPORTER NUMBER OF SEQUENCES: 9
                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acid
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REGISTRATION NUMBER: 36,688
REFERENCE,DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO PILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                         COUNTRY:
                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
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CAO, LIANG
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01-MAR-1995
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Best Local S
Matches 105
                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                      Sequence 2, Application US/09139675A Patent No. 6117426
APPLICANT: Li, Yi
APPLICANT: Cao, Liang
APPLICANT: Rosen, Craig
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A
CURRENT FILING DATE: 1998-08-25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/894,840
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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NAME: STEFFE, ERIC K
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KYIFGLTIPSYTGP--GSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARY 276
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                                                                                             APPLICANT: Xu, Hong
APPLICANT: Cohan, Victoria L.
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEI
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: PF-0550 US
CURRENT APPLICATION NUMBER: US/09/110,116
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09110116 Patent No. 6013479 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: WO PCT/US95/02645
EARLIER FILING DATE: 1995-03-01
EARLIER APPLICATION NUMBER: US 08/471,496
EARLIER FILING DATE: 1995-06-06
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: UNSURE
LOCATION: (402)
OTHER INFORMATION: May be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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                                          ENGTH: 886
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mes 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLAVDGAG--GKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PESAKGTPLFMLLKDPYILVAAGSI---C----FANMGVAILEPTLPIWMMQTMCSPKW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MQFGFVAIYLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PPPATEAISAHKNNCLQGTGFLEEETTRVGVLFAS-KAVMQLLVNPFVGPLTNRIGYHI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRLLKEGRASRQLVLVVVFVALLLDNMLFTVVVPIVPTFLYDMEFKE-VISSLHLGHAGS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKLRNAFRCSSAKIKAVVFGLL------PVL-SWLPKYKIKDYIIPDLLGGLSGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLGLAFLPASVSYLIGTNLFGVLANKMGRWLCSLIGMLVVGTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHKIR----FPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KYIFGLTIPSYTGP--GSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQM------GLGF-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S---PHALA-----SPAFSTIF-SFFNNNTV----AVEESVPSGIAWMNDTASTI---- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGTALGGLALGLLVGAPFGSVMYEFVG--KSAPFLILAFL--ALLDGALQLCILQPSKVS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMFAGFVIMFLSTVMFAFSGTYTLLFVARTLQGIGSSFSSVAGLGMLASVYTDDHERGRA
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Pred. No. 0.0015;
0; Mismatches 184;
                                                                                                                                                                                                    PROTEIN COUPLED
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RESULT 8
US-08-843-417-10
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; OTHER INFORMATION: 784994, GenBank
US-09-110-116-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
TELEFAX: (415)-324-063
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                               TELEPHONE: (415)-324-7041
                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 NTET 748
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                                                                                  REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                 APPLICATION NUMBER: US/08/8 FILING DATE: April 15, 1997
                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GRTLANKHGYDVDSNQEMTALGC----SNFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10, Application US/08843417
o. 6184349
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                                                                                                                                                                                                                                                                                                                                         CA
                                                                                                                                                                                                                                                                                                                                                                          525 University
                                 (415)-324-0638
                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delgado, Stephen G
Fish, Linda M
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                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                        Heller Ehrman White & McAuliffe
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20.7%;
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Pred. No. 0.32;
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                                                                                                                                                                                                                       Version
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; TYPB: amino acid
; STRANDEDNESS: unkn
; TOPOLOGY: unknown
; MOLECULE TYPE: pepti
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-843-417-10
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US-08-677-049-9
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                                                                                                                                                                                                                                                                        Sequence 9, Application US/08677049 Patent No. 5858707 GENERAL INFORMATION:
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                                                                                                                                 APPLICANT: Guimaraes, M. Jorge
APPLICANT: Bazan, J. Fernando
APPLICANT: McClanahan, Terrill K.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1013 GGEDAQSFQQEVIPKGQQEQLQQVERCGDHLTP-----RSPGTGTSSEDLAPSLGETWK 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 YFANSEIFROKVIAK--TVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 QMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLA--CL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 HVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKN 444
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STATE: California
COUNTRY: USA
                                                            STREET:
                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSSKAENHIAANTARGSSGGLQAPRGPRDEHSDFIANPTVWVSVPIAEGESDLDDLEDD
                                                                                                                                                                                                                                                                                                                                                                                                                    DESVPQAPAEGVDDTSSSEGSTVDCLDPEEILRKIP 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SLKQLTDPYYLWRKSKLDCCIWVVSF-----LSSFF-LSLPYGVAVGVAFSVLVVV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFPIPTEMIVVV----VATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQSEPPASAEAPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQTQFRNGYALAQVM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNLTIILATIVFVFAL-VGKQLL----GENYRNNRKNISAPHEDWPRWHMHDFFHSFLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIAL-----GCSNFFGSFFKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWNIFDCIIVTVSLLELGVAKKGSLSVLRSFRLLRVFKLAKSWPT-LNTLIKIIGNSVGA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GL--TIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKI 280
                                         T: 901 California Avenue
Palo Alto
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                                                                                    DNAX Research Institute
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NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 244; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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LOCATION: 359..386
COTHER INFORMATION: /r.
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LOCATION: 115..144

OTHER INFORMATION: /
OTHER INFORMATION: 4:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region LOCATION: 323..357 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
   471
                                  323
                                                                                                                                   369
                                                                                                                                                                                                   314
                                                                                                                                                                                                                                   177
                                                                                                 270 YRAEGLAVLLGGIFN-----AFPYT-AFSQNVGLVQLTGIKKNAVIVVTGVILMAFGLF
                                                                                                                                                                                                                                                                                                 121 FPPVVTGSVVTIIGITLMPVAMN----NMAGGEGSADFGDLSNLALAFTVLSIIVLLYRF 176
                                                                                                                                                                                                                                                                                                                                 232 TGP---GSIV----FTFIDICKNLPHTNIA-------SLIFALISGAFL----
                                                                                                                                                                                                                                                                                                                                                                                               172 VSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                  74 LGCTFTAVSPMIAIG---SEYGVSTVY------GSIIASG--ILVILISFFFGKLV-SF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/000,788 FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 2.78;
Local Similarity 19.68;
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TOPOLOGY: li
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                                                                                                                                                                                     EIQRGFPT-PVSPVVSQWKDMIGTAFSLAIVSYV----INLAMGRTLANKHGYDVDSNQE 368
                                                                                                                                                                                                                                 TKGFIKSVSILIGILIGTFIAYFMGKVQFDNVSDAAVV--
                                                                                                                                  MIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIY-LY
                                                                                                                                                                  PFYFGAPSFHAAPII-----TMSIVAIVSLVESTGVYFALG-DLTNRRLTEIDLSKG 269
                                  PKIAAFTTIIPSAVLGGAMVAMFGMVIAYGIKMLSRIDFAKQENLLIVACSVGLGLGVTV
                                                               P-----LPKSVI.G----ALIAVNLKNSLKQLTDPYYLWRKSKL--DCCIWV---VSF
                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
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                                                                                                                                                                                                                                                                -----VLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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 YGVAVGVAFSVLVVVFQTQFRNGYALAQVMD
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103; DB 2; 1
Pred. No. 0.14;
6; Mismatches 132;
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US-08-861-464-4
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 140; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senescence
TITLE OF INVENTION: in Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patticia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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TOPOLOGY:
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247 NLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKK 306
                                            199
                                                                                    193
                                                                                                                       140 SVTPAASLRNFSNSNNAASKCGVDNSSFGLSS-STSSSMVEISALPLRDLDYIKLATDQF 198
                                                                                                                                                    STREET: Two Mil
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                 93 ALLANLPAVNGLYSSFFPLLTYFFL--GGVHQMVPGTFAVI------SILVGNICL 140
                                                                                                                                                                                                            87 ASMANPPAI-----LPLINEFDLEMDGPRRKSSHDFTVVAPSNSGVNTSSLIMETPSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                  G--FVAIYL---SES-FIRGEMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICK 246
                                       GCRFLQKKLETPSESNMVRDLMYEQIKPFFLDLILDPFG-----NYLVQKLCD 246
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                            2.7%; Score 103; DB 2; Length 834; 17.6%; Pred. No. 0.41; tive 110; Mismatches 294; Indels 2
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                                                                                                                                                                                                                                                                                              Indels 250;
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                    192
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	: 28-FEB-1995 ION: 435	
	RENT APPLICATION DATA: DDI.TCATTON NUMBER: 115/08/395 001	
	PERATING SYSTEM: PC-DOS/MS-DOS	
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	
	READABLE	· · ·
	RY:	
	CITY: Lexington STATE: MA	
	STREET: Two Militia Drive	
	ONDENCE ADDRESS:	
	٥ ب	
	INVENTION: Gen	
	APPLICANT: COIE, ridnoesca APPLICANT: Kennedy, Brian	
	: Claus, James	
	nte, Leo iaco Jr.	
	ORMATION:	
	ULT 11 08-396-001-4 equence 4, Appli	US
	780 YQTEGANWDSSLSM 793	Db
	710 HNFQGAPGDAELSL 723	Qy
779	731TNVNPNVSRGFKQPGFMMNETDKINANHFSPYSNANSQNENESFVPRMQ	Db
709	658 KVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDVTPG	Qy
730	672 MNENQNAYPSMGAPSFNSQTNPPLVS-HNSLQNFDNRQFANLMAHPNSAAPIHSESSSNI	ДЬ
657	604SAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGV	Qy
671	612 NHNHNHAHNNNNNNNQKSHTRHESLPANAYHRRSNSSYTNNFSNQYAQDQKIHSPQQI	DЬ
603	INQTPANGTSVSYIT	Оу
611	552 PSIKTTSYAKKIKLKVKAYAEATGIPFTDISPQVTAMSHNULQTINNENKNPHNKNSHNH	Db
566	529IKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFEN	Qy
551	493 GN-YALQTLLDVKNYSPLLAYNKNSNAIGQNSSSTLNYGNFCNDFSLKIGNLIVLTKELL	Ф
528	500 RNGYALAQVMDTDIYVNPKTYNRAQDIQG	Qy
492	433 EKFIKKLFRIITGFIVNUNGGASQRTAVASDDVINASMNILLTTIDIFTVNLNVLIRDNF	Ъ
499	473 SFFLSLPYGVAVGVAFSV-LVVVFQTQF	Qy
432	386 NDQFGNYIIQFLLDIKELDFYLLAELFNRLSNELCQLSCLKFSSNVV	Db
472	YPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCC	Оу
385	337 DAIVEQNNITTISTHKHGCCVLQKLLSVCTLQQIFKISVKIVQFLPGLI	Db
421	364 DSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLV	Qy
336	295KGFSQEFTSIEQVVT	Db
363	VVSQWKDM	Qy
294	247 YLTAEQKTLLIQTIYPNVFQISINQYGTRSLQKIIDTVDNEVQIDLII	DЪ

; TOPOLOGY: 11; MOLECULE TYPE: US-08-396-001-4

linear

protein

Matches 140;

87

TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid

TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240 TELEFAX: 617-861-9540

ATTORNEY/AGENT INFORMATION:

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Query Match 2.7%; Score 103; DB Best Local Similarity 17.6%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 QLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFM-----QF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 YHMQIVGEIQRGFP---TPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 SYTPAASLRNESNSNNAASKCGYDNSSEGLSS-STSSSMVEISALPLRDLDYIKLATDQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ALLANLPAVNGLYSSFFPLLTYFFL--GGVHQMVPGTFAVI-------SILVGNICL 140
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2
                                                                                                                                                   MNFNQNAYPSMGAPSFNSQTNPPLVS-HNSLQNFDNRQFANLMAHPNSAAPIHSFSSSNI
                                                  ----TNVNPNVSRGFKQPGFMMNETDKINANHFSP-----YSNANSQNFNESFVPRMQ 779
                                                                                              KVFLVNIHAQVYNDISHGGVF--EDGSLECKHVFPSIHDAVLFAQANARDVTPG-----
                                                                                                                                                                                                                                              NHNHNHAHNNNNNNNQKSHTRHFSLPANAYHRRSNSSVTNNFSNQYAQDQKIHSPQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LGIYLYPLPKSV-----LGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DS--NQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLV 421
                                                                                                                                                                                                                                                                                                                                                 PSIKTTSYAKKIKLKVKAYAEATGIPFTDISPQVTAMSHNNLQTINNENKNPHNKNSHNH
                                                                                                                                                                                                                                                                                                                                                                                                                                               GN-YALQTLLDVKNYSPLLAYNKNSNAIGQNSSSTLNYGNFCNDFSLKIGNLIVLTKELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNGYALAQVMDTDIYVNPKTYNRAQDIQG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFFLSLPYGVAVGV-----AFSV-LVVVFQTQF 499
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                                                                                                                                                                                                 --SAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGKIGV
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; SEQ ID NO 4
; LENGTH: 834
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-323-433A-4
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US-09-323-433A-4
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Best Local Similarity
Matches 140; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050.1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1994-08-15
PRIOR APPLICATION NUMBER: US 08/107,4C
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version
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GN-YALQTLLDVKNYSPLLAYNKNSNAIGQNSSSTLNYGNFCNDFSLKIGNLIVLTKELL
                                                                                              EKFIKKLFRITTGFIVNNNGGASQRTAVASDDVINASMNILLTTIDIFTVNLNVLIRDNF
                                                                                                                                                SFFLSLPYGVAVGV---
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Cole, Francesca
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1994-08-15
IUMBER: US 08/107,408
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                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,729
APPLICATION NUMBER: 29-JUN-1993
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: E
FILING DATE: 11-JUN-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patent In Re
CURRENT APPLICATION DATA:
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                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                              FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and
NUMBER OF SEQUENCES: 31
                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                   APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/627,950
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
                                                                        TELEFAX:
                                                                                                                           REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
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LENGTH:
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                                                       66441 PENNIE
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                                                                        (212) 869-8864
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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14-DEC-1990
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11-JUN-1993
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Avenue of the Americas
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                                                                                                                                             18,872
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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
NAME: Livnat, Shmuel 33,949
REGISTION NUMBER: 33,949
REFERENCE,DOCKET NUMBER: MEI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MERUELO, DANIEL APPLICANT: YOSHIMOTO, TAKAYUI TITLE OF INVENTION: Human Rei TITLE OF INVENTION: Therefor
                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304
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                                                                                                                                                                                                                                                                                                                                             STREET: 419 Sever CITY: Washington
                                                                                                                        APPLICATION NUMBER: POFILING DATE: 19921213
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                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV-ICCALSVTLAVDGAGGKSQVASLCVSLV------VMITMLVLGIYLYPLPKSVLGAL 437
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                                                                                                                                              PCT/US92/09382
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                   MERUELO-1
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Best Local S
Matches 96
                                                                                                                                                                                          APPLICANT: Burnham, Martin
APPLICANT: Lonetto, Michael
APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL TETRACYCLINE RESISTANCE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08898976 Patent No. 5891670
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                 ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
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TYPE: AMINO ACID
STRANDEDNESS: single
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LENGTH: 622 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 LVYQMARTTEELDRVDQNELVSASESQTGFLPVAEKFSLKSILSPKNVEPSKFSGLIVNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 CLQLAPESKFQVFNNATNESYVDTAAMEAERLHV-SATLACLTAIIQMGLGFMQFGFVAI 197
                                                                                                                                                                    STATE: N

/ Match 2.6%;
Local Similarity 20.5%;
hes 96; Conservative 60

APPLICATION NUMBER:
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us/08/898,976
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Pred. No. 0.4;
0; Mismatches 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
403
                                                                                                                                                                                                                                                                                                                                                                                                  111 SPUTLVGRIIQTAGLAAAETLYVIYVAKYLSKEDQKTYLGLSTSSYSLSLVIGTLSGGFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 PLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER 169
                                                                             351
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                                     389 CALSVTLAVDGA------GGKSQVASLCVSLVVMITMLVLGIYLY
                                                                                                                                                                                                   302 KMPKKYHMQI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 LNISVTTVSWQATLAGLV-IGMGAVVYASLSDAISIRPPFIYGVILIIFGSIIGNIFQHQ 110
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VAVSVGIAIAAALIDFKALNFPGNDALSSHFGIILIILGLMSIVGLVLF
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                                                                             AVGNHISIFVISMIFFAGSFALMYAPLLNEAIKTIDLNMTGVAIGFYNL-----IIN 402
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                                                                                                                   SLA--IVSYVINL------AMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVIC 388
                                                                                                                                                           IMEQIYHLQLDTTSLLLVPGYIVAVIVGALSGKIGEYLNSKQAIITAIILIALSLILPAF 350
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                                                                                                                                                                                                 -----VGEIQRGFPTPVSPVVSQWKDMIGTAF 338
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Gaps

19;

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301 230

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Search completed: April 26, Job time: 203 sec 2002, 09:05:37

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Database
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Soybean sulphate p	Peptide #1699 enco Human polypeptide Wheat sulphate per	Peptide #1706 enco Peptide #1774 enco	Rat DTDST protein. Human DTDST protei	Human membrane tra Down-requlated in	Description

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AAY44938	AAY37263	AAM33220	AAM19798	AAB07557	AAB42187	AAB76816	AAG91372	AAG82493	AAW98528	AAY44937	AAY95728	AAB40320	AAG03678	AAB76818	AAG90717	AAG83019	AAG32202	AAG29249	AAG32201 ·	AAG31622	AAG29248	AAE04904	AAG90917	AAB76817	AAY44358	AAY44359	93	AAY44944	AAY44942	AAG31620	AAG32200	31	AAG29247
Artichoke sulphate	ia trac	Peptide #7257 enco		Protein encoded by	Human ORFX ORF1951	Corynebacterium gl	C glutamicum prote	S. epidermidis ope	H. pylori GHPO 141	Corn sulphate perm	Cosmid cHRIM5 enco	Human ORFX ORF84 p	Human secreted pro	Corynebacterium gl	C glutamicum prote	Ω.	Arabidopsis thalia	Arabidopsis thalia			Arabidopsis thalia	Human transporter	C glutamicum prote	Corynebacterium gl	P. chrysogenum sut	P. chrysogenum sut	Corn sulphate perm		phate			tha	Arabidopsis thalia

ALIGNMENTS

AAY71067 RESULT AAY71067 standard; Protein; 29-AUG-2000 AAY71067; ب (first entry) 758

Human membrane transport protein, MTRP-12.

Human; membrane transport protein; MTRP-12; antiinflammatory; cytostatic; antithyroid; immunosuppressive; thyromimetic; antidabetic; noctropic; antidiarrheic; neuroprotective; antidepressant; nephrotropic; virucide; antihelminthic; protozoacide; antibacterial; neuroleptic; antigout; diagnosis; prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzheimer's disease; depression; schizophrenia; immune disorder; allergy; inflammatory disorder; ALDS; Addison's disease; atherosclerosis; gout; Graves disease; Hashimoto's thyroiditis; microbial infection; cancer; cell proliferative disorder

Homo sapiens

	Modified-site	Modified-site	Modified-site	Modified-site	Key Modified-site
/note=	/note= 574	/note= 376	/note= 251	/note= 174	Location 138
<pre>/note= "Phosphorylation site"</pre>	"Phosphorylation site"	"Phosphorylation site"	<pre>/note= "Phosphorylation site" 251</pre>	/note= "Phosphorylation site" 174	Location/Qualifiers 138

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04-NOV-1998;
24-NOV-1998;
22-DEC-1998;
26-FEB-1999;
                                                                                         The present sequence is a membrane transport protein,
MTRP-12 from Incyte clone 1733477 isolated from human BRTTUT08 cDNA
Library, MTRP-12 shows homology to mouse transporter (GI 5359730)
and human transporter (GI 291964), and is expressed in nervous,
and human transporter (GI 291964), and is expressed in nervous,
gastrointestinal and reproductive tissues.
The present sequence is useful in diagnosis, prevention and treatment
of disorders related with increased or decreased expression of MTRP
such as familial goitre, Menkes disease, diabetes, Parkinson's disease,
such as familial goitre, Menkes disease, diabetes, Parkinson's disease,
           neurological disorders such as Alzheimer's disease, depression, epilepsy, schizophrenia, immune/inflammatory disorders such as AIDS, Addison's disease, allergies, atherosclerosis, Graves disease, gout, Hashimoto's thyroiditis, viral, bacterial, fungal, parasitic, protozoal or the infections and cell proliferative disorders such as cancer. Fragments of MTRP polynucleotides are useful as targets in microarrays. MTRP DNA is also useful for generating hybridisation probes useful in
                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                       Claim 1; Page 105-106;
                                                                                                                                                                                                                                       Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorder
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Matches 259
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                                                                                                                                    --TVSLQELQQDFE----
                 IGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDV
                                                 edatanggedskap-dgstlkalglpqpdfhslildlgalsfvdtvclkslknifhdfre
                                                                                                         qeqlklkqlqkeeklrkqaaspkgasvsinvntsledmrsn---nvedckmmvssgdkm
                                                                                                                                                              diyrdvaeyseakevrgvkvfrssatvyfanaefysdalkqrcgvdvdflisqkkkllkk
                                                                                                                                                                            PYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDT
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                                                                                                                                                                                                                                                                                        SYTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTD
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                                                                                                                                                                                                                                                                                                                                               {\tt Indklqqqlpmpipgelltligatgisygmglkhrfevdvvgnipaglvppvapntqlfs}
                                                                                                                                                                                                                                                                                                                                                                                                   LNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWK
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ievevymaachspvvsqleaghff-dasitkkhlfasvhdavtfalqhprpv
                                                                               SPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGIKALAKLSSTYGK
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Pred. No. 2.1e-118;
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                                                                                                                                    -NAPPTDPNNNQTPANGTSVSYITFSPDSS
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RESULT
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Down-regulated
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              down-regulated in adenoma; t
n adenocarcinoma; diagnostic;
                                                                                  standard; Protein;
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                                    in
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                                    DRA tumor suppressor
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide that is adenocarcinomas and adenomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 25-27; 41pp;
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nes 249; Conserv
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                                                                                                 LTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIV
                                                                                                                                                                          rlkewlisdivsgistgivavlqglafallvdippvyglyasffpaiiylffgtsrhisv
                                                                                                                                                                                                 KIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVP 125
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                     GGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANK
                                                                                                                               gpfpilsmmvglavsgavskavpdrnattlglpnnsnnsslldd---ervrvaaaasvtv
                                                                                                                                                     GTFAVISILVG----NICLOLAPESKFQVF---NNATNESYVDTAAMEAERLHVSATLAC
ygcdfknrfkvavvgdmnpgfqppitpdvetfqntvgdcfgiamvafavafsvasvyslk
                                           kvlysvfsqiektniadlvtalivllvvsivkeinqrfkdklpvpipiefimtviaagvs
                                                                FTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAIS
                                                                                     lsgiiqlafgilrigfvviylseslisgfttaaavhvlvsqlkfifqltvpshtdpvsif
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573..580
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Pred. No. 7.9e-104;
42; Mismatches 275;
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transporter expression containing a DNA sequence encoding a mammalian containing no DNA sequence of 5' translation region of the mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing

for

containing

This invention describes the construction of a novel vector for sulfate

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Best Local S
Matches 219
DTDST; human. expression vector; bone disease; cartilage disease; drug preparation.
                                                           Human DTDST protein
                                                                                           19-AUG-1999
                                                                                                                                                   AAY08928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence represents the rat DTDST protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                -lelhtvvidcsaiqfldtagihtlkevrrdyeaigiqvllaqcnpsvrdslakgey---
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31.7%; Pred. No. 1.7e-89;
tive 140; Mismatches 280;
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                sulphate transporter; screening;
treatment; cell sulphate ion int
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Matches 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes the construction of a novel vector for sulfate transporter expression containing a DNA sequence encoding a mammalian sulfate transporter (expression product of the DTDST gene) and containing no DNA sequence of 5' translation region of the mammalian sulfate transporter gene. The invention also describes; (A) a method for screening a human bone/cartilage disease treating agent including the steps: (1) transforming an animal cell with the above vector, (2) culturing the animal cell in the presence of a sample and (3) detecting the increase in the sulfate ion intake to the cell; (B) a drug preparation for the treatment of human bone/cartilage disease containing the above vector as the active component. The sulfate transporter gene-containing vector is high in expression efficiency. This sequence represents the human DTDST protein used in the method of the invention.
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htqlsgvvtalvlllvlavlaplfyslqksvlgvitivnlrgalrkfrdlpkmwsisrmd
                     KSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLD
                                                                     igfaitvslsemfakkhgytvkangemyaigfcniipsffhcfttsaalaktlvkestgc
                                                                                                                                                        TEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWK---DMIGTAFSLAI
                                                                                                                                                                                                                                                                                                                                                                              HQMVPGTFAVISILVGNIC---LQ------LAPESKFQVFNNATNESYVDTAAM 165
                                                                                                                                                                                                                                                                                                                                                                                                            wlpkydlkknilgdvmsglivgillvpqsiaysllagqepvyglytsffasilyfllgts
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                                                                                                      VSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGG
                                                                                                                                    ielvvvvaatlashfgklhenynssiaghiptgf---mppkvpewnlipsvavdaiaisi
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226; Conserv
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31.2%; Pred. No. 3e-8
tive 138; Mismatches
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No. 3e-89;
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CCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNR

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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                    The present invention relates to human single exon nucleic acid probes (SEMP: see AAI10068-AAI28459). The present sequence is a peptide encode by one such probe. The SEMPs are derived from human HeLa cells. The SEM can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefor useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM15272 standard; Protein;
                                   specification, but was obtained in
                                                                                                                                                                           Claim
                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                         WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001 (first entry)
                       at ftp.wipo.int/pub/published_pct_sequences
                                               Note: The sequence data for this patent did not
                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer.
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                                                                                                                                                                          27; SEQ ID No 20098; 487pp; English.
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                                                                                                                                                                                                                                                               Hanzel
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2000US-0608408.
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                                                                       from human cervical probes are therefore cervix, notably
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                    21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                 30-JAN-2001;
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                                                                                                                                                                                                              genetic disorder
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Local Similarity 31.2%;
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                    2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-02346359.
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%; Pred. No. 1.6e-65;
105; Mismatches 212;
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Best Local S
Matches 164
 Probe; human; breast disease;
inflammatory disease; prolifer
                                                                    AAM03017;
                           Peptide #1699 encoded by probe for measuring breast gene expression
                                                  09-OCT-2001
                                                                                       AAM03017 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                          VNIHAQVYNDISHGGVFEDGSLECKH----VFPSIHDAVLFAQAN 702
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zing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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31.2%; Pred. No. 1.6e-65;
disease; breast cancer; developeroliferative breast disease;
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         development
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 non-carcinoma
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          disorder;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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         llvgvcfsifcvilrtqkpkssllglveesevfesvsayknlqtkpgikifrfvaplyyi
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast cancer, disorders proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2001; 2001WO-US00661
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                                               Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                      19.0%;
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                                            0%; Score 735.5; DB 22
2%; Pred. No. 1.6e-65;
105; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe used
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                                                                                                DB 22;
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                                                 45;
                                                 Gaps
244
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185 MGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                VAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFA
                                                                                                                                                                                                                             enynssiaghiptgf---mppkvpewnlipsvavdaiaisiigfaitvslsemfakkhgy 177
                                                                                                                                                                                                                                                                                                                    DVDSNQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLV
                                            iaplfyslqksvlgvitivnlrgalrkfrdlpkmwsisrmdtviwfvtmlssallsteig
                                                                    LGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYG
                                                                                                                                   tvkanqemyaigfcniipsffhcfttsaalaktlvkestgchtqlsgvvtalvlllvllv
                                                                                                                                                                                                                                                                            KKYHMQIVGEIQRGFPTPVSPVVSQWK----DMIGTAFSLAIVSYVINLAMGRTLANKHGY
                                            297
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RESULT
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                                                                                      31-JAN-2000;
04-FEB 2000;
19-MAY-2000;
11-MAY-2000;
11-AUGL-2000;
11-AUGL-2000;
11-SEP-2000;
06-SEP-2000;
08-SEP-2000;
25-SEP-2000;
25-SEP-2000;
08-NOV-2000;
13-OCT-2000;
08-NOV-2000;
18-NOV-2000;
18-NOV-2000;
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18-NOV-2000;
19-NOV-2000;
11-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
18-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM42394 standard;
                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155449-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological disease; infection; nephrotropic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
Rosen
                      (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 agcnptvrdsltngey-----ckkeeenllfysvyeamafaevs 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEP
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Barash
                                                                                                                                                 2000US-0249211.
2000US-0249214.
2000US-0249265.
                                                                                                                                                                                             2000US-0246525.
2000US-0246526.
2000US-0246528.
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2000US-0239937.
2000US-0246476.
2000US-0246477.
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                                                                                                                                                                                                                                                                                                    2000US-0230437
                                                                                                                                                                                                                                                                                                                                                  2000US-0216880
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                      GENOME
SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 143
                      SCI INC
MS
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, funguand parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
                                                                                                                                                                                    mapping; marker; plant breeding; chimeric
antibody; screen.
                                                                                                                                                                                                  Sulphate Permease; sulphate assimilation protein; wheat; probe; mapping; marker; plant breeding; chimeric gene; transgenic plan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAI62752-AAI62961) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
               14-JUL-1998;
                                               13-JUL-1999;
                                                                                                                  WO200004154-A2
                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                   Wheat sulphate permease-2.
                                                                                                                                                                                                                                                                                       23-MAY-2000
                                                                                                                                                                                                                                                                                                                        AAY44945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                 27-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 SFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAME 166
                                                                                                                                                                                                                                                                                                                                                                                                                                        129 gqepthswprsiaf 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                     (first entry)
              98US-0092833
                                               99WO-US15810
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91.0%;
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                                                                                                                                                                                                                                                                                                                                                            593
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Pred. No. 8.9e-53;
3; Mismatches 8
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                                                                                                                                                                                                    plant;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence is the wheat sulphate permease, a sulphate assimilation protein. This sequence is obtained from wim4 library, clone wim4.pk0016.all, derived from wheat seedlings, 4 hours after inoculation with E. graminis. It has 73% sequence identity to Arabidopsis thallana sulphate permease (gi 2626753). This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant breeding and to construct chimeric genes, used to create transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid fragments encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding homologous proteins, in producing transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants with altered levels of sulphate permease. The sulphate permease peptides are useful for producing antibodies, that are used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6;
                                                               454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolate cDNA clones
snrgpdvg--
                               NNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSG
                                                                            savnhesgaktglsgiimgiiicsallfmtplftdipqcalaaiv-isavtglvdyeeai
                                                                                                                                                                                                                                                       mptailitgvailesvgiakalaakngyeldsnkelfglglsnicgsffsaypatgsfsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLGGVHOMVPGTFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSAT
                                                             yrntlqypeaytyngivvvrvdapiyfanisyikdrlreyelkl-
                                                                                                                       {\tt flwgidkkdfflwamtftttltfgieigvlvgvgfslafvihesanphiavlgrlpgttv}
                                                                                                                                                        YLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDI
                                                                                                                                                                                                                        TLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPY
                                                                                                                                                                                                                                                                                     IGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSV
                                                                                                                                                                                                                                                                                                                                                   RYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQRGFPT-PVSPVVSQWKDM
                                                                                                                                                                                                                                                                                                                                                                                 pliesiiagidqfswppfvmgsaflvillimkklgktn-kklrflrasgpltavv-----
                                                                                                                                                                                                                                                                                                                                                                                                                ------IPSYTGP----GSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 59-60; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 576; DB 21;
Pred. No. 3.2e-49;
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                                                                                                                                                                                                                                                                                                                 -vvgeipqglpsfsiprgfehlmsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 593;
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518
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Qy DЬ Q

LSWLPKYKIKDYIIPDLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLG 118

fewapkytfq-flkadliagitiaslaipqgisyaklanlppilglyssfippliyammg

PRPRYYVDRAAYSL--TLEDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGL---LPV 58

pppqpffkslkyslketffpddplrqfknkpaskkf--

-mlglqfffpi

92

Matches

Conservative

128;

4

Query Match Best Local Similarity

14.68;

Score 566; DB 21; Pred. No. 4.1e-48; 8; Mismatches 293;

Length

Indels 132;

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                                                            The present amino acid sequence is the soybean sulphate permease, a sulphate assimilation protein. This sequence is obtained from sfl1 library, clone sfl1.pk0043.910, derived from soybean immature flower. It has 75% sequence identity to Arabidopsis thaliana sulphate permease (g1 2285885). This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is
                     useful for plant breeding and to construct chimeric genes, used to create transgenic plants with altered levels of sulphate permease. The sulphate permease peptides are useful for producing antibodies, that are used to screen and isolate cDNA clones.
                                                                                                                                                                               Sequence
                                                                                                                                                            Claim
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sulphate assimilation protein. This sequence is from a country composed of clones cbn10.pk0062.b10, ccoln.pk081.h21, ccoln.pk092.12, csclc.pk005.j3, p0004.cblej58r, p00089.csdch19r, p0094.csssg12r, p0121.cfrmx30r and p0128.cpicz09r from cbn10, ccoln, csclc, p0004, p0089, p0094, p0121 and p0128 libraries, respectively. It has 80.2% sequence identity to Sporobolus stapfianus sulphate permease(gi 197270). This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant breeding and to construct chimeric genes, used to create transgenic plants with altered levels of sulphate permease. The sulphate permease paptides are useful for producing antibodies, that are used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid fragments encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding homologous proteins, in producing transgenic plants -
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N-PSDB; AAZ50481.
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                                                                    WRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDTDIYV
                                                                                             {\tt vnynagcktamsnivmaiavmftllfltplfhytplvvlsaii-isamlglidyqaaihl}
                                                                                                           AVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYL
                                                                                                                                       l:: |::| :| ::| |::| | ::| |::| |::| :: | ::
tglitgiialaegvavgrsfamfknynidgnkemiafgmmnivgsftscylttgpfsrsa
                                                                                                                                                  TAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSFFKIHVICCALSVTL
                                                                                                                                                                             aamapltsvilgsllvyfthaerhgvqvigdlkkgl-nplsgsdliftspyms---tavk
                                                                                                                                                                                        VATA----ISGCKM----PKKYHMQIVGEIQRGFPTPV------SPVVSQWKDMIG
                                                                                                                                                                                                                    dstdvisvmrsvfsqthewrwes---gvlgcgflffl--lstry----fsikkpkffwv
                                                                                                                                                                                                                                         GPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVV
                                                                                                                                                                                                                                                           aftatffagvleaslgifrlgfivdflshativgfmggaatlvslqqlkgifgl--khft
                                                                                                                                                                                                                                                                         SATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYT : | : | | | | | : : | | | | | | : : |
                                                                                                                                                                                                                                                                                                                                                                                 PRPRYVVDRAAYSL--TLF-DDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGL---LP
                   ntegypssrtvpgilileidapiyfanasylreriirw---
                             NPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKVIAKTVSLQELQQDFENAPPTDPNNN
                                                       wkvdkfdflvcmsayvgvvfgsveiglvvavaisiarlllfvsrpktavkgnipnsmiyr
                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; al Similarity 24.9%; 180; Conservative 12:
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99US-0159339
99US-0159330
99US-0159537
99US-0159638
99US-0160741
99US-0160767
99US-0160778
99US-016078
99US-0160814
99US-0160814
99US-0160981
99US-0161405
99US-0161405
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S-0161992.
S-0161993.
S-0162142.
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S-0159584.
S-0160741.
S-0160767.
S-0160768.
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s-0159329.
s-0159330.
s-0159331.
s-0159637.
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Pred. No. 7.5e
27; Mismatches
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RESULT
25 FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
24-MAR-1999
16-APR-1999
16-APR-1999
11-APR-1999
21-APR-1999
21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction hybridisation assay; genetic mapping; gene (termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG32200 standard; Protein;
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990S-0127462
990S-0128214
990S-01280714
990S-01300479
990S-0130510
990S-0131449
990S-0132407
990S-0132486
990S-0132486
990S-0132486
990S-0132486
990S-0134219
990S-0135124
990S-0135124
990S-0135124
990S-0135124
990S-0135124
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99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
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expression control;
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promoter;
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Query Match
Best Local Sim
Matches 180;
                                                        09-AUG-1999
10-AUG-1999
11-AUG-1999
12-AUG-1999
12-AUG-1999
12-AUG-1999
13-AUG-1999
13-AUG-1999
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13-AUG-1999
13-AUG-1999
14-AUG-1999
15-SEP-1999
16-SEP-1999
17-AUG-1999
17-AUG-1999
18-AUG-1999
19-AUG-1999
19-AUG
               Similarity
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99US-0149684
99US-0149175
99US-0149175
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99US-0149723
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99US-0151066
99US-0151066
99US-0151066
99US-0151066
99US-0151067
99US-0151067
99US-0151069
99US-0161160
                14.0%;
24.9%;
Score 543.5; I
Pred. No. 7.5e
27; Mismatches
                  .5e-46;
                              DB.
                              21;
                           Length
                               658
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Conservative

127;

274;

Indels 141;

Gaps

23;

08-JWN 1999
110-JWN 1999
110-JW

990S-0138094
990S-013919
990S-0139450
990S-0139451
990S-0139456
990S-0139451
990S-0139451
990S-0139451
990S-0139461
990S-0139461
990S-0139461
990S-014081
990S-014082

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RESULT 1
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                                                EP1033405-A2
                                                                                                                                                                  Arabidopsis thaliana protein fragment
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                  06-SEP-2000
                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                       634
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::
::
                                                                                                                     genetic
                                                                                                                     signal transduction pathway; metabolic
netic mapping; gene expression control;
                                                                                                                                                                   SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----vdaekdpklylhl 166
                                                                                                                                                                   38003.
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                                                                                                                     promoter;
                                                                                                                                     pathway;
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          AVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALIAVNLKNSLKQLTDPYYL
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Search completed: April 26, 2002, 09:05:16 Job time: 207 sec

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